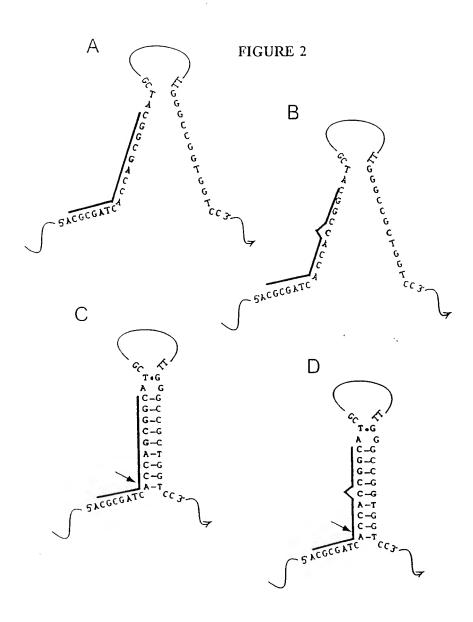


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FIGURE 3

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FIGURE 4



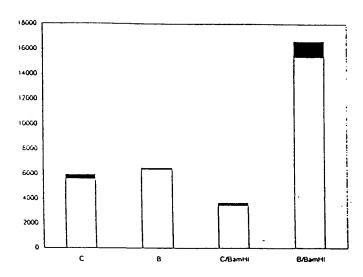
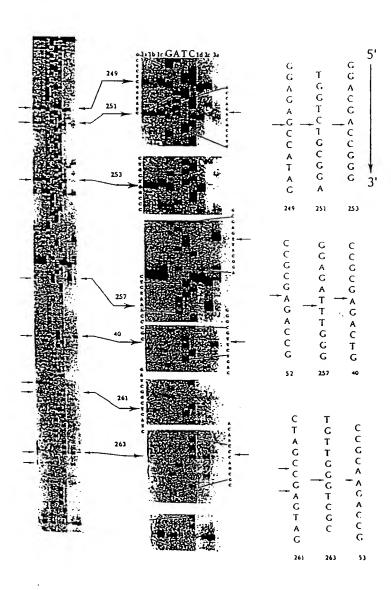


FIGURE 5



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FIGURE 6

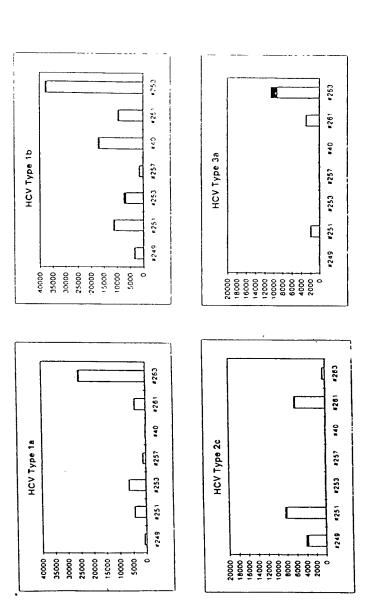
Consensus:GATTCTGTCT TCACGCAGAA AGCGTCTAGC CATGGCGTTA GTATGAGTGT CGTGCAGCCT HCV 1a	TACACCGGAA	#253 TTGCCAGGAC GACCGGGTCC TTTCTTGGAT CAACCCGCTC AATGCCTGGA GATTTGGGCG	#40 #263 TGCCC <u>CCGCA AGACTGCTAG CCGAGTAGTG TTGGGTCGC</u> G AAAGGCCTTG TGGTACTGCC	
GTATGAGTGT	#251 TGGTCTGCGG AACCGGTGAG	#257 AATGCCT <u>GGA_GATTTGGG</u>	AAAGGCCTTG	CGTGCAATC
CATGGCGTTA	#251 TGGTCTGCGG	TTTCTTGGAT CAACCCGCTC AATGCCTGGA GATTTGGGC	#263 <u>rc TTGGGTCGC</u> G	TCTCGTAGAC
AGCGTCTAGC	#249 CCAGGACCCC CCCTCCCGGG AGAGCCATAG	TTTCTTGGAT	#2 CCGAGTAGTG	TGATAGGGTG CTTGCGAGTG CCCCGGGAGG TCTCGTAGAC CGTGCAATC
TCACGCAGAA	CCCTCCCGGG	#253 TTGCCA <u>GGAC GACCGGG</u> TCC	#40 #261 CCCCCCA AGACTGCTAG	CTTGCGAGTG
GATTCTGTCT	CCAGGACCCC	#253 TTGCCAGGAC	#40 TGCCC <u>CCGCA</u>	TGATAGGGTG
Consensus HCV la HCV lb HCV 2c HCV 3a				

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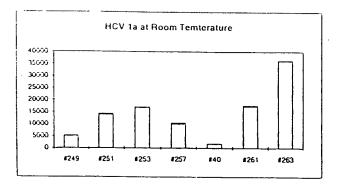
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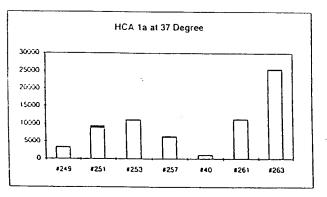
FIGURE 7

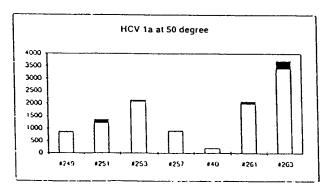


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FIGURE 8A

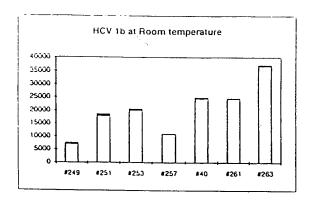


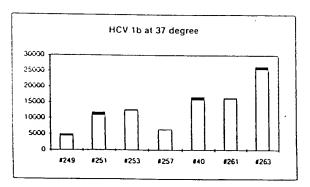




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FIGURE 8B





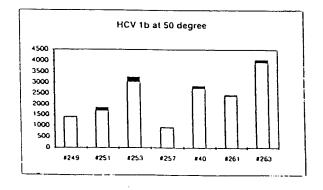
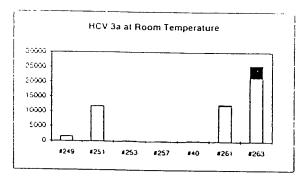
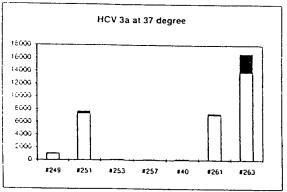


FIGURE 8C





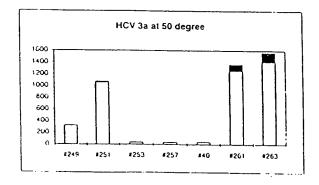


FIGURE 9A

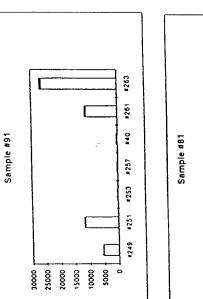
TOBBEOKS . SAISOL

#263 •261 Sample #69 Sample #85 **#**257 #253 #249 12000 10000 6000 4000 #263 #261 07.8 Sample #73 Sample #72 #253 \$0000

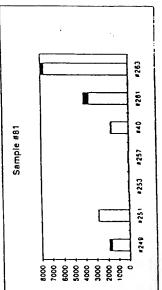
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.263 152 40 Sample #95 1257 F253

FIGURE 9B



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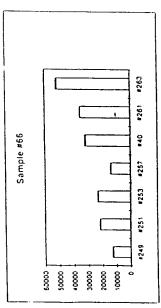
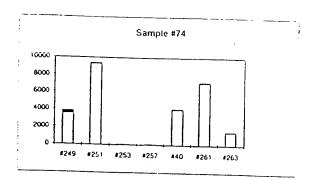


FIGURE 9C

FIGURE 9D



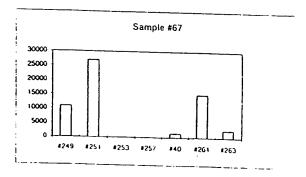


FIGURE 11A .

#2) 5' Biotin

T A
C G A
A T — A
G C — G
A T — A
C G — C
A T — A
G C — G
C G — C
G C — G

#80) 5' - FI-TGCTCTCTGGT TGGTCTCTCGTAAT-3'

4 FD91) 3' Biotin - C G A G A G A C C A - 5'

A G A A C — G — C C — G — C C — G

#80) 5' - FI-TGCTCTCTGGT TGGTCTCTCGTAAT-3'

#78) 3' - A G A C C A T T A C C A G A -Biotin 5'

#4) 3' - G A G A C C A T T A C C A G A G -Biotin 5'

#79) 3' - A G A G A C C A T T A C C A G A G A -Biotin 5'

VV

#116) 3' - A G A G A C C A A C C A G A G A -Biotin 5'

#117) 3' - T A C C A G A G A -Biotin 5'

#118) 3' - A G A G A C C A T - 5'

FIGURE 11B

$$G \qquad A$$

$$T \rightarrow A$$

$$C \rightarrow G$$

$$T \rightarrow A$$

$$G \rightarrow C$$

$$T \rightarrow A$$

$$C \rightarrow G$$

$$G \rightarrow C$$

$$C \rightarrow G$$

$$G \rightarrow C$$

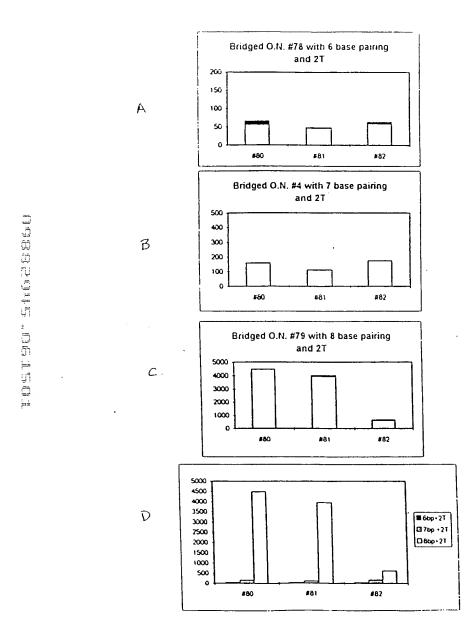
$$T \rightarrow G$$

$$G \rightarrow C$$

$$G \rightarrow G$$

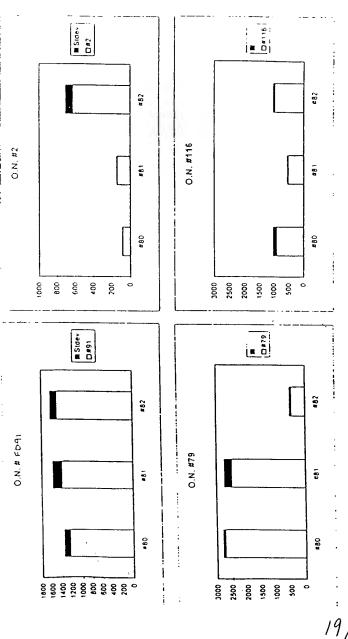
$$G \rightarrow$$

FIGURE 12



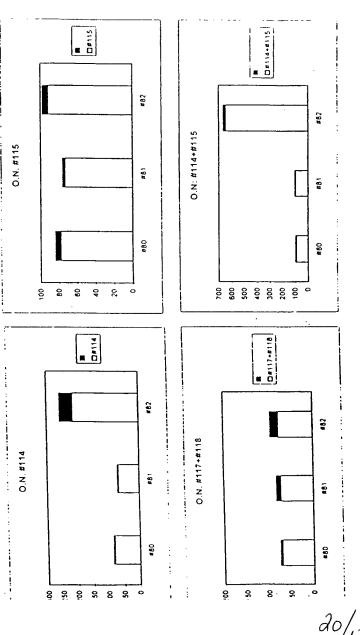
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FIGURE 13A



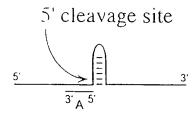
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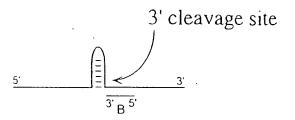
FIGURE 13B

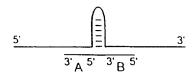


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FIGURE 14







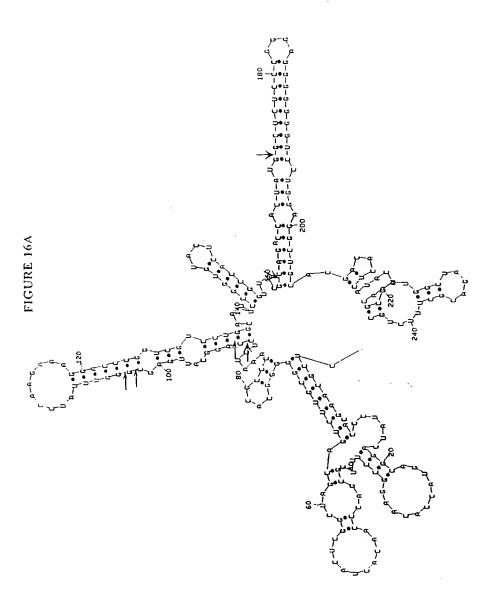
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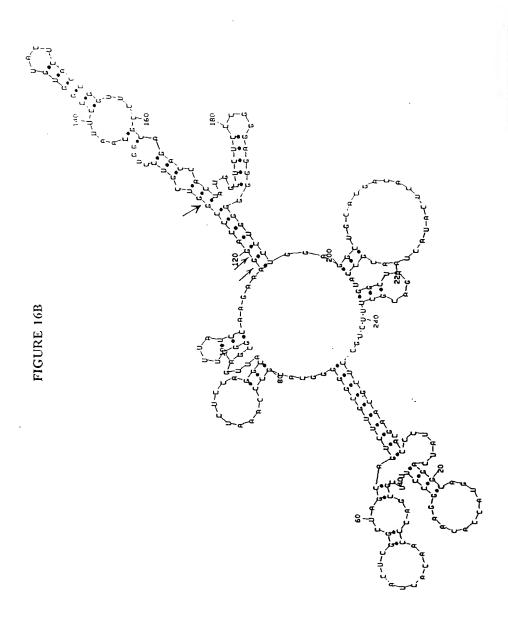
FIGURE 15

	1102030
1a	
ŧ	
2a/c	2a/c
3a	TGAC
	90100110120130140150160
1	18 cccaaatctcbalgggattgaggbgggtttatccaagaaaldgagggggggggggggggggggggggggggg
đ	
2a/c	
3a	3aT. Htcl. TGTGT
	2.
19	18 GEAGACCACTATHECTCCCGGGAGGGGGGGGTCCTGGAGGCTGCACGACACTCATACTAACGCCATGGCTAGACGCTTTTCTGC
đ	10 J.
2a/c	2a/c
3a	3a [

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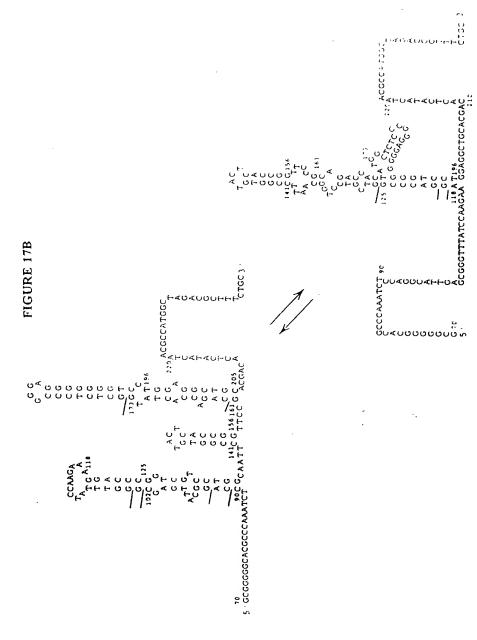


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FIGURE 17A



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FIGURE 17C

5 Biotin

M (#81-04)3'-AGGTTCTT_{CC} CCTCCGAC-F]-5

FIGURE 18A

```
HCV 1a
                                                         G G
G A
                                                          \mathsf{C}\,\mathsf{G}
                                CCAAG

T A

A T G

T G
                                                          CG
                                                          CG
                                                          ΤG
                                                          CG
                                                          ΤG
                                   TA
                                                          СG
                                   G C
                                                          GТ
                                   G C
                                                       173 G C
A T 196
                                G C
102C G 125
G G
A T
                                                          ТG
                                                          C G
A A
                                   \mathsf{G}\ \mathsf{C}
                                 A_{C\ G\ C}^{T^T\ G} T
                                                          CG
                                                          C G
                                                         A<sub>G</sub> C
                                    GC
                                                          ΑТ
                                    ΑT
                                                СG
                                    CG
                                                          \mathsf{C} \; \mathsf{G}
5 -TGCGGGGCACGCCCAAATCT CAATT TTCC ACGACACT 3
                          (179-49-01)3· GGCC\overline{\mathtt{AAGG}}_{TT}\overline{\mathtt{TGCTGTGA}}5· b
                          (192-72-01)3 · GGCCAAGG AA TGCTGTGA 5 · |
                          (192-72-02)3 · GGCCAAGGACTGCTGTGA 5 · |
                           (192-72-03)3 · GGCCAAGG —TGCTGTGA 5 · K
                          (192-72-04)3 · GGCCTAGG_{TT}TGCTGTGA 5 · C
                           (192-72-05)3 · GGCCAAGG TT TGCAGTGA 5 · C
```

FIGURE 18B

HCV 1b	G G G A C G
TCCAAGA A A G G G T G T G T A A A G G G T A G G G G G G G G G G G G	C G C G C G C G T G T G C G G T 173 G C T C A T 196 T G A C C G T C C G T A C C C G T A C C C G T A C C C C C C C C C C C C C C C C C C
	GGCCAAGG TT TGCTGTGA 5. b
(192-72-01)3	GGCCAAGG AA TGCTGTGA 5 1
(192-72-02)3	GGCCAAGG AC TGCTGTGA 5
(192-72-03)3	GGCCAAGG —TGCTGTGA 5 · K
(192-72-04)3	GGCCTAGG TT TGCTGTGA 5. C
(192-72-05)3	GGCCAAGG _{TT} TGCAGTGA 5 · Q

FIGURE 18C

```
AAG
C A
C A118
AT A
T G
                     HCV 2a/c
                          GGA
GGG
CG
CG
          ТG
          TA
          \mathsf{G}^{\mathsf{C}}
          G C
          G C
                           {\tt T} \; {\sf G}
       102 T A125
GA TG
                           CG
                           тG
          G C
                           CG
         ATATOGC
                           G C
                        173 G C 196
T<sub>A T</sub>
     (179-49-01)3 \cdot \text{GGCCAAGG}_{TT} \overline{\text{TGCTGTGA}} 5 \cdot b
(192-72-01)3 · GGCCAAGG AA TGCTGTGA 5 · |
(192-72-02)3 · GGCCAAGG AC TGCTGTGA 5 · |
(192-72-03)3 · GGCCAAGG —TGCTGTGA 5 · K
(192-72-04)3 · GGCCTAGG TT TGCTGTGA 5 · C
(192-72-05)3 · GGCCAAGG TT TGCAGTGA 5 · d
```

FIGURE 18D

```
HCV 3a
               CAAG
C A
T A
                                    G \stackrel{G}{\sim} G
                 T A 118
                                    GCG
                G G
                 ТG
                                       C G
                  A T
                  G C
                                        C G
                  \mathsf{G}\;\mathsf{C}
                                        тG
                  \mathsf{G} \; \mathsf{C}
                                        C G
              102C G 125
G G
A T
                                        тG
                                        СТ
                                       \mathsf{G}\,\mathsf{C}
                  G C
                                    173 G C
               A_{\mathbf{T}GC}^{\mathbf{T}\mathbf{A}\mathbf{A}}C
                                      T<sub>A T 196</sub>
                                        ΤG
                                      C G A A C G C G A G C
                  GC AC
GC T T
                90CG TA
TrgC GC
TGC GC AT

TA GC AT

AT CG CG

AT CG CG

AT CG CG

ACGACACT

CACGCCCA

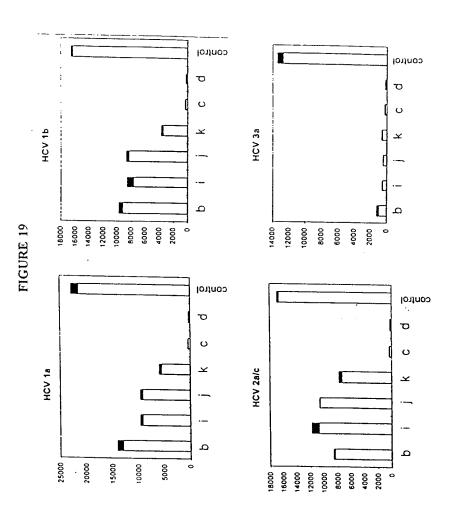
TTCC

ACGACACT

(179-49-01) 3 · GGCCAAGG

TTCCTGTGA 5 · D
(192-72-01) 3 · GGCCAAGG AA TGCTGTGA 5 · |
(192-72-02)3 GGCCAAGG AC TGCTGTGA 5
(192-72-03)3 · GGCCAAGG —TGCTGTGA 5 · K
(192-72-04)3 · GGCCTAGG<sub>TT</sub>TGCTGTGA 5 · C
(192-72-05)3 · GGCCAAGG TT TGCAGTGA 5 · d
```





FICHRE 20A										-										
	ບ ້) (O	90	TG	. ·	76	90	FO	173.6.0	HCV 1a	, O	<u> </u>	A A	ပပ	90'	A G C	TK	90	G C 205 C C C C C C C C C C C C C C C C C C C	AATTCCGGTGTACTCACCGGIICC ACGACACI - 3
																				1

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F1.5 (192-72-04)

3 - GGCCTAGG TT TGCTGTGA

3 - GGCCAAGG TT TGCAGTGA F1 .5 (192-72-05)

3 - - GGCCAAGG - F15 - (205-27-01)

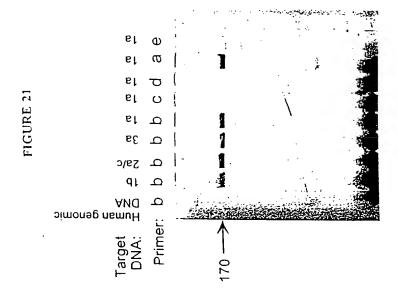
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31-GGCCAAGGCGTCTGGTGA-F1.5. (205-13-02) A

3 - GGCCAAGG TT TGCTGTGA F1 5 (179-49-01)

FIGURE 20B

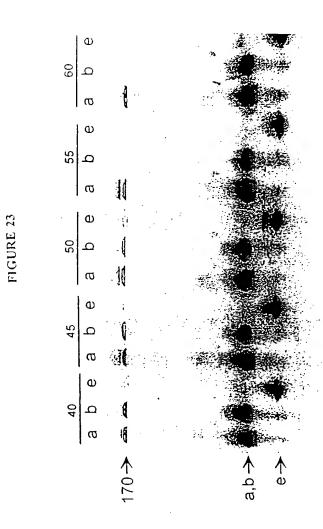


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FIGURE 22		3. 1.5.(205-13-02 1.5.(179-49-01) -01)
ი ი ი ი ი ი ი ი ი ი ი ი _დ ი ი ი ი ი ი ი ი ი	HCV 1a 1200 TO A A D D A D D A D D A D D D D D D D D	-caattccggtgtactcaccggttcc ^{G C} ACGacact-3 3 - <u>ggccaag</u> cgtctg <u>gtga</u> -F1 5 (205-13- 3 - <u>ggccaagg _{tt}tgctgtga</u> .F1 5 (179-49-0

 σ

D 0



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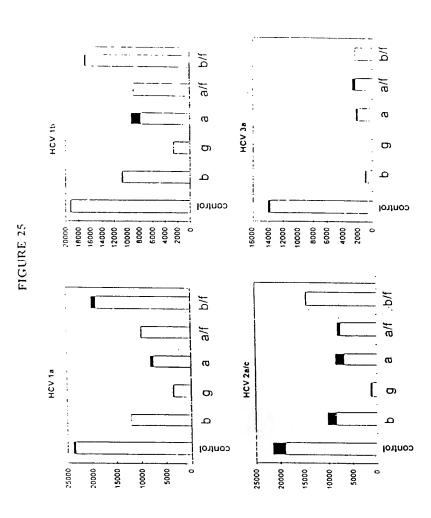
FIGURE 24 G G C C T G C G T G C G T G C G T G C G A T C G C G C G C G C G C G C G C		3 - GGCCAAGG TTTGCTGTGA F1 . 5 · (179-49-01) D	3'-GGCCTAGG _{TT} TGCTGTGA" F1'5'(192-72-04) C
--	--	--	--

 \circ σ Φ

3 - - GGCCAAGG-F15 (205-27-01)

3 - - GGCCAAGG TT TGCAGTGA

F1 'S' (192-72-05)



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FIGURE 26

3 - GGCCAAGGCGTCTGGTGA-F1 . 5 · (205-13-02) A Φ 5 - ATTCCGGTGTACTCACCGGTTCCAAACGACACT-3 ' (205-13-01) S.T. \circ ∇ $3 \cdot - \texttt{GGCCAAGG}_{TT} \\ \texttt{TGCTGTGA} \cdot \cdot \texttt{Fl} \cdot \texttt{5} \cdot (179 - 49 - 01)$ $3 \cdot - \texttt{GGCCTAGG}_{TT} \\ \texttt{TGCTGTGA} \\ - \cdots \\ \texttt{Fl·5} \cdot (192 - 72 - 04)$ 3 - GGCCAAGG TT TGCAGTGA F1 . 5 . (192-72-05) 3 - - GGCCAAGG-F15 (205-27-01) f (192-96-01)3 - TAAGGCCACATGAGT-5

FIGURE 27

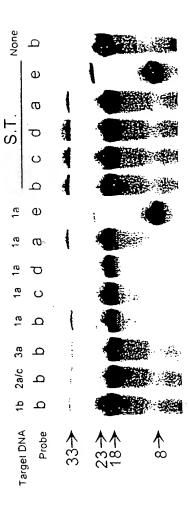
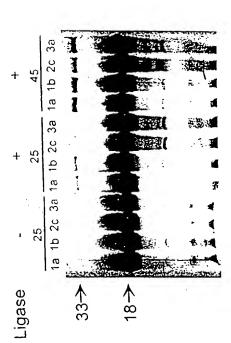


FIGURE 28



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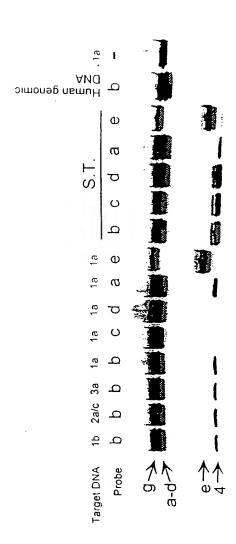
		σ	9	\circ	σ	Φ	
G G FIGURE 29A CG CG FIGURE 29A CG CG TG CG TG CG TG CG TG CG TG CG CG TG CG	TO A T196 TO CO CO A D A CO CO CO CO CO CO CO CO CO CO	5. (205-13-02)	(179-49-01)	3 - GGCCTAGG TT TGCTGTGA F1 · S · (192-72-04)	3 - GGCCAAGG TTTGCAGTGA F1 · S · (192-72-05)	CAAGG-F15'(205-27-01)	3TAAGGCCACATGAGTG _T T _T Fl.5.(192-96-02)
							D

DOODESTE LIGHTS

FIGURE 29B

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FIGURE 30



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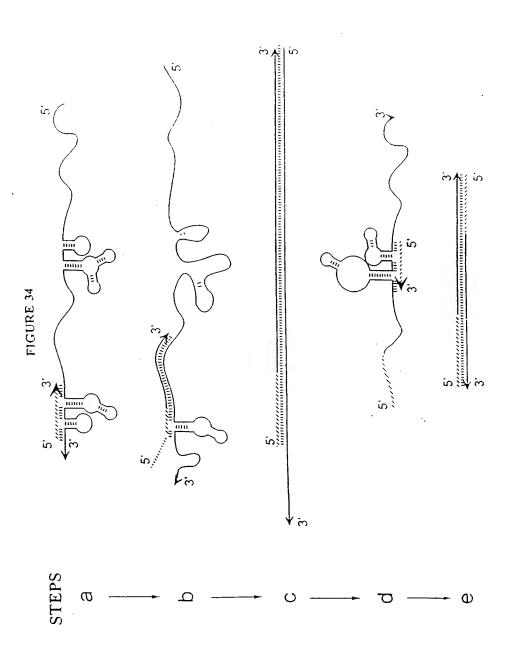
	Ω
G G FIGURE 31 C C C C C C C C C C C C C C C C C C C	CG CG CG AGC AT CG TCACCGGTTCC GC205ACACT 3 ' 3 - GGCCAAGG TTGCTGTGA · F1 · 5 · (179 - 49 - 01) AGTG TT
HCV 1a	CG CG CG CG CG CG CG CG CG AT CG CG S.—CAATTCCGGTGTACTCACCGGTTCCG CACGACACT 3GGCCAAGG TTTGCTGTGA.F1. h (10 bp)3'-CACATGAGTG TTTTTTTTCTGGCTGA.F1)

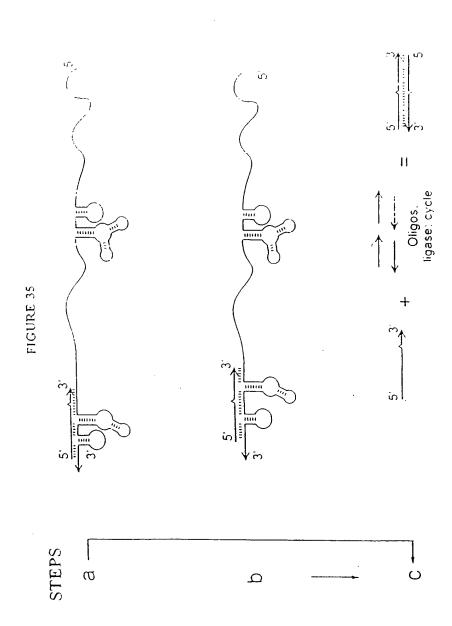
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FIGURE 32

			$\sqrt[4]{\sqrt{1}}$	7	†
	1	3а		!	1003
		1b 2a/c 3a	11	1	1915
Q	30	10	44	- 1	1918
		٦ م	3	1	2085
		3a		1	1608
٠ د	35	1b 2a/c 3a	5	1	2421
		10		1	2583
		1a	3	1	2960
		3a	E	•	872
_	2	1b 2a/c	13	1.	1298
יב	45	₽	41	ŧ	1324
		<u>a</u>		1	1605
		3a	3		(1068)
	_	1b 2a/c 3a	3		
l	30	2 2	3		
		1a			
Probe	Temp	Target			

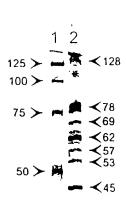
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FIGURE 36



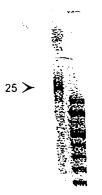
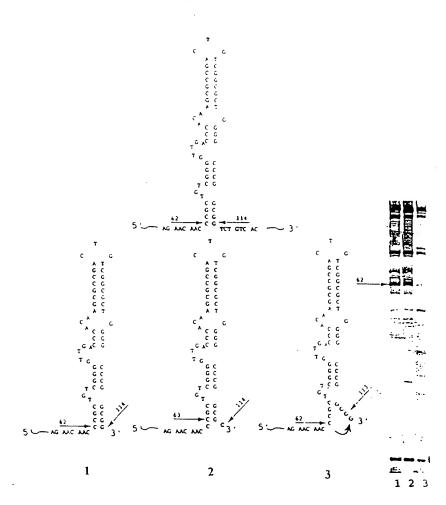


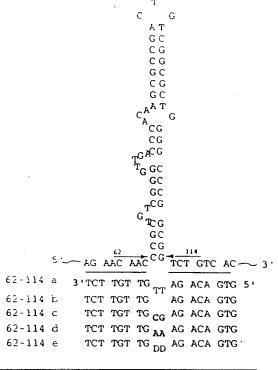
FIGURE 37A

FIGURE 37B



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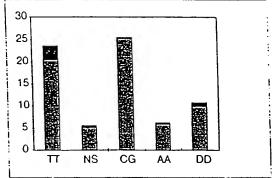
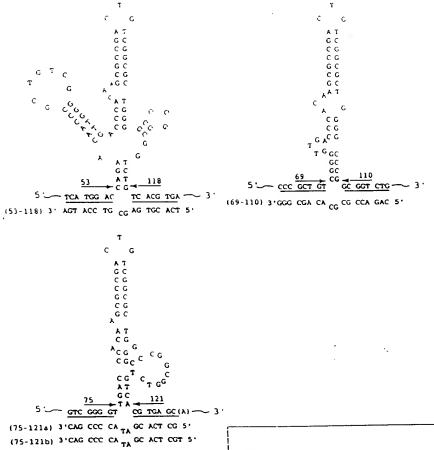
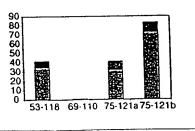
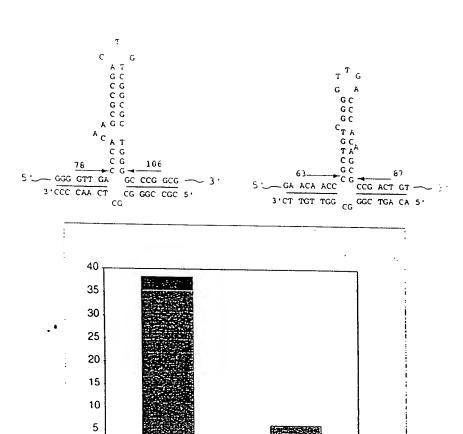


FIGURE 38A



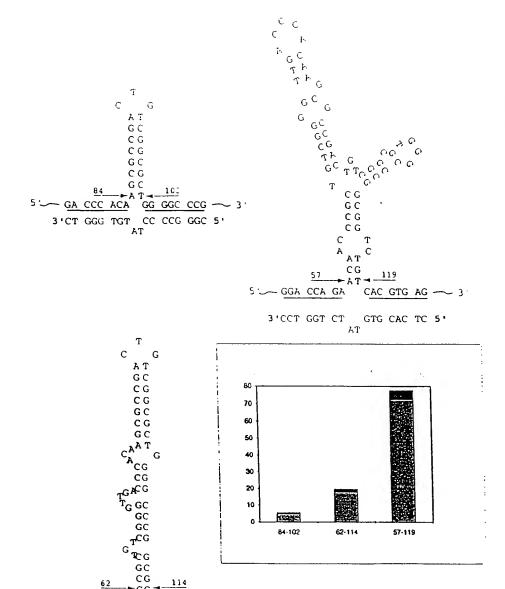






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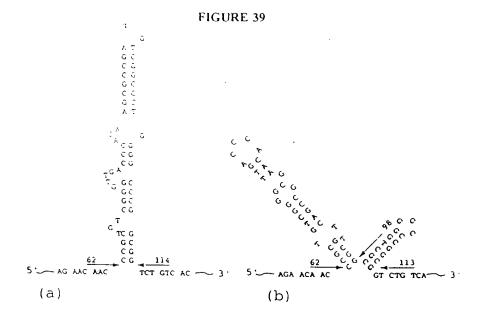


 $- \underset{ACA}{\text{AGA}} \underset{ACA}{\text{ACA}} \underset{AC}{\text{CG}} \underset{TCT}{\underbrace{114}} \underset{GTC}{\text{AC}} \longrightarrow 3$

3'TCT TGT TG AGA CAG TG 5'

. Littles -





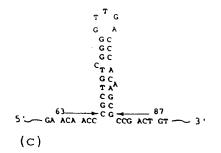
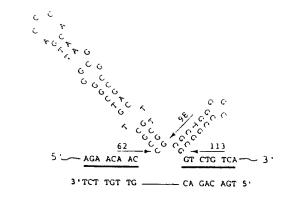


FIGURE 40



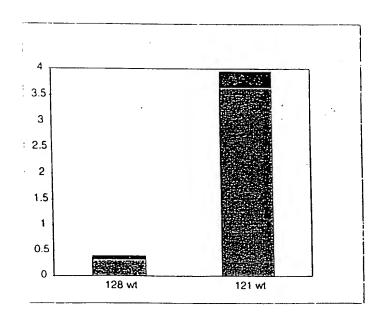
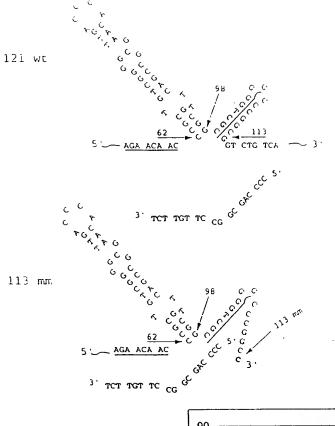


FIGURE 41



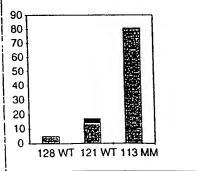
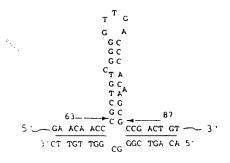
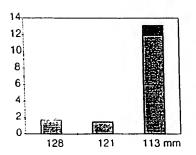


FIGURE 42





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FIGURE 43A

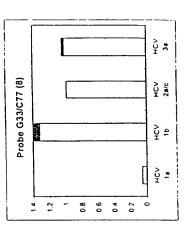
FIGURE 43B

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3 . - GGTGTTC GT TGCGGGT -- F1-5' G33-C77(7)

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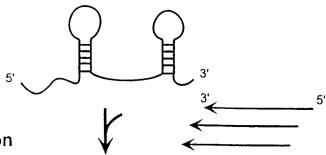
FIGURE 44A



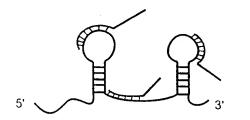
namaraka looksor

0.045
0.045
0.045
0.045
0.035
0.035
0.025
0.005
0.005
0.005
0.005
0.005
0.006

FIGURE 44B



I) Hybridization



II) Reverse Transcription

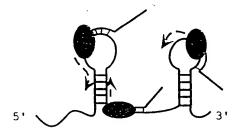
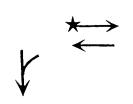
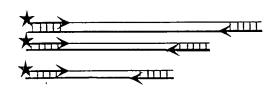




FIGURE 45A



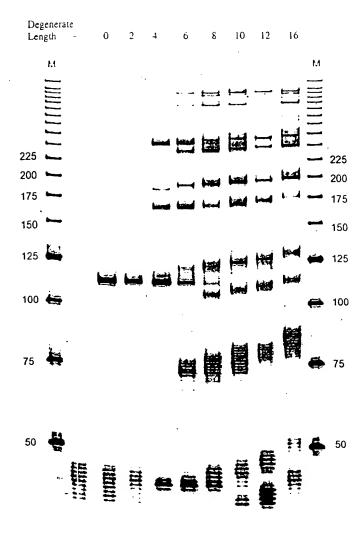
III) PCR





IV) PAGE with Sequencing Ladder

FIGURE 45B



•,.

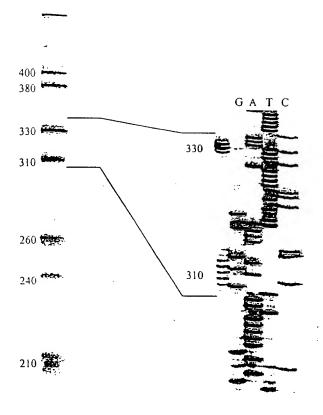
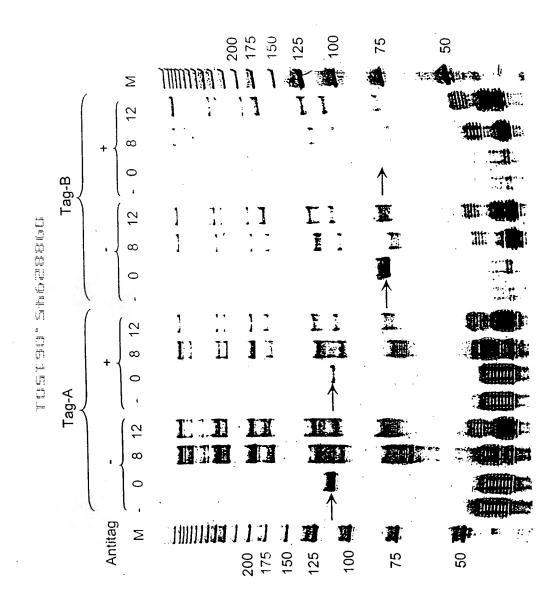


FIGURE 47



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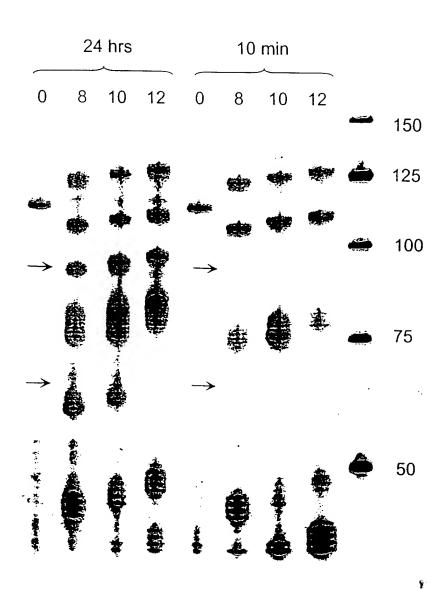


FIGURE 49

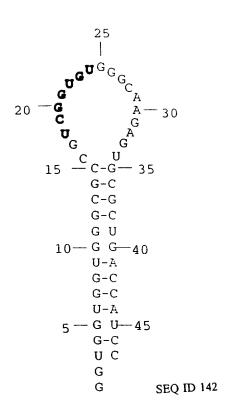
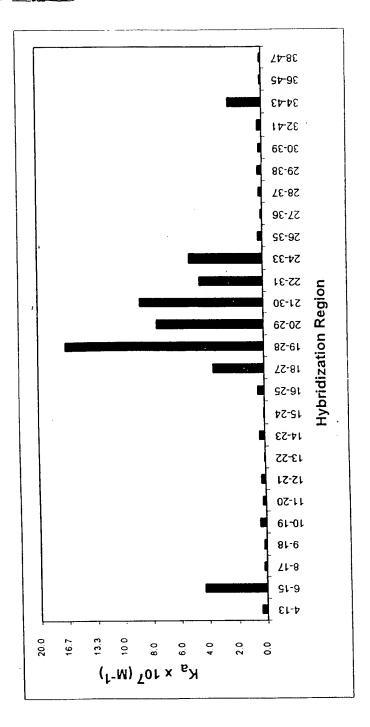


FIGURE 50A





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L	ACACUUGCUU	UUGACACAAC	UGUGUUUACU	44-50 UGCAAUCCCC	CAAAACAGAC
51	64-68 AGA AUGG UGC	AUCUGUCCAG		38-97 UCUGCGGUCA	CUGCCCUGUG
01	GGGCAAGGUG	AAUGUGGAAG	AAGUUGGUGG	UGAGGCCCUG	GGCAGGCUGC
151	UGGUUGUCUA	CCCAUGGACC	CAGAGGUUCU	UCGAGUCCUU	UGGGGACCUG

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: IGURE 52A

ISIS 1571(-) ISIS 3067(+)
1 GCGCCCCAGT CGACGCTGAG CTCCTCTGCT ACTCAGAGTT
ISIS 1570(+)
41 GCAACCTCAG CCTCGCTATG GCTCCCAGCA GCCCCCGGCC
81 CGCGCTGCCC GCACTCCTGG TCCTGCTCGG GGCTCTGTTC
121 CCAGGACCTG GCAATGCCCA GACATCTGTG TCCCCCTCAA
161 AAGTCATCCT GCCCCGGGGA GGCTCCGTGC TGGTGACATG
201 CAGCACCTCC TGTGACCAGC CCAAGTTGTT GGGCATAGAG
OAA TATAAAAAAA OMAAAAAA OMAAAAAAAAAAAAAA
241 ACCCCGTTGC CTAAAAAGGA GTTGCTCCTG CCTGGGAACA
281 ACCGGAAGGT GTATGAACTG AGCAATGTGC AAGAAGATAG
281 ACCGGAAGGI GIAIGAACIG AGCAAIGIGC IMGIMGIMIG
ISIS 1934(-)
321 CCAACCAATG TGCTATTCAA ACTGCCCTGA TGGGCAGTCA
321 00.2.00.2.10
361 ACAGCTAAAA CCTTCCTCAC CGTGTACTGG ACTCCAGAAC
401 GGGTGGAACT GGCACCCCTC CCCTCTTGGC AGCCAGTGGG
AAA ONDONE DOCCEDACCOM COODCOMOCA CCOMOCCOCA
441 CAAGAACCTT ACCCTACGCT GCCAGGTGGA GGGTGGGGCA
481 CCCCGGCCCA ACCTCACCGT GGTGCTGCTC CGTGGGGAGA
401 CCCCCCC VICTORIOGE COLORED COLORED

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1 - 3URE 52B

521 AGGAGCTGAA ACGGGAGCCA GCTGTGGGGG AGCCCGCTGA as 610 561 GGTCACGACC ACGGTGCTGG TGAGGAGAGA TCACCATGGA 601 GCCAATTTCT CGTGCCGCAC TGAACTGGAC CTGCGGCCCC 641 AAGGGCTGGA GCTGTTTGAG AACACCTCGG CCCCCTACCA 681 GCTCCAGACC TTTGTCCTGC CAGCGACTCC CCCACAACTT 721 GTCAGCCCCC GGGTCCTAGA GGTGGACACG CAGGGGACCG 761 TGGTCTGTTC CCTGGACGGG CTGTTCCCAG TCTCGGAGGC 801 CCAGGTCCAC CTGGCACTGG GGGACCAGAG GTTGAACCCC 841 ACAGTCACCT ATGGCAACGA CTCCTTCTCG GCCAAGGCCT 881 CAGTCAGTGT GACCGCAGAG GACGAGGGCA CCCAGCGGCT 921 GACGTGTGCA GTAATACTGG GGAACCAGAG CCAGGAGACA 961 CTGCAGACAG TGACCATCTA CAGCTTTCCG GCGCCCAACG 1001 TGATTCTGAC GAAGCCAGAG GTCTCAGAAG GGACCGAGGT

1: JRE 52C

1041 GACAGTGAAG TGTGAGGCCC ACCCTAGAGC CAAGGTGACG 1081 CTGAATGGGG TTCCAGCCCA GCCACTGGGC CCGAGGGCCC 1121 AGCTCCTGCT GAAGGCCACC CCAGAGGACA ACGGGCGCAG 1161 CTTCTCCTGC TCTGCAACCC TGGAGGTGGC CGGCCAGCTT as 1220 (+) 1201 ATACACAAGA ACCAGACCCG GGAGCTTCGT GTCCTGTATG 1241 GCCCCGACT GGACGAGAGG GATTGTCCGG GAAACTGGAC 1281 GTGGCCAGAA AATTCCCAGC AGACTCCAAT GTGCCAGGCT 1321 TGGGGGAACC CATTGCCCGA GCTCAAGTGT CTAAAGGATG ISIS 1547 (+) 1361 GCACTTTCCC ACTGCCCATC GGGGAATCAG TGACTGTCAC 1401 TCGAGATCTT GAGGCCACCT ACCTCTGTCG GGCCAGGAGC 1441 ACTCAAGGGG AGGTCACCCG CGAGGTGACC GTGAATGTGC 1481 TCTCCCCCG GTATGAGATT GTCATCATCA CTGTGGTAGC 1521 AGCCGCAGTC ATAATGGGCA CTGCAGGCCT CAGCACGTAC

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1561 CTCTATAACC GCCAGCGGAA GATCAAGAAA TACAGACTAC as 1630 as 1630h(+++) 1601 AACAGGCCCA AAAAGGGACC CCCATGAAAC CGAACACACA ISIS 1938 (+) 1641 AGCCACGCCT CCCTGAACCT ATCCCGGGAC AGGGCCTCTT 1681 CCTCGGCCTT CCCATATTGG TGGCAGTGGT GCCACACTGA 1721 ACAGAGTGGA AGACATATGC CATGCAGCTA CACCTACCGG 1761 CCCTGGGACG CCGGAGGACA GGGCATTGTC CTCAGTCAGA 1801 TACAACAGCA TTTGGGGCCCA TGGTACCTGC ACACCTAAAA 1841 CACTAGGCCA CGCATCTGAT CTGTAGTCAC ATGACTAAGC 1881 CAAGAGGAAG GAGCAAGACT CAAGACATGA TTGATGGATG ISIS 1939 (+) 1921 TTAAAGTCTA GCCTGATGAG AGGGGAAGTG GTGGGGGAGA 1961 CATAGCCCCA CCATGAGGAC ATACAACTGG GAAATACTGA 2001 AACTTGCTGC CTATTGGGTA TGCTGAGGCC CACAGACTTA 2041 CAGAAGAAGT GGCCCTCCAT AGACATGTGT AGCATCAAAA

URE 52E

ISIS 2302 (+) 2081 CACAAAGGCC CACACTTCCT GACGGATGCC AGCTTGGGCA 2121 CTGCTGTCTA CTGACCCCAA CCCTTGATGA TATGTATTTA ISIS 1572 2161 TTCATTTGTT ATTTACCAG CTATTTATTG AGTGTCTTTT 2201 ATGTAGGCTA AATGAACATA GGTCTCTGGC CTCACGGAGC 2241 TCCCAGTCCA TGTCACATTC AAGGTCACCA GGTACAGTTG 2281 TACAGGTTGT ACACTGCAGG AGAGTGCCTG GCAAAAAGAT 2321 CAAATGGGGC TGGGACTTCT CATTGGCCAA CCTGCCTTTC 2361 CCCAGAAGGA GTGATTTTTC TATCGGCACA AAAGCACTAT 2401 ATGGACTGGT AATGGTTCAC AGGTTCAGAG ATTACCCAGT 2441 GAGGCCTTAT TCCTCCCTTC CCCCCAAAAC TGACACCTTT 2481 GTTAGCCACC TCCCCACCCA CATACATTTC TGCCAGTGTT 2521 CACAATGACA CTCAGCGGTC ATGTCTGGAC ATGAGTGCCC 2561 AGGGAATATG CCCAAGCTAT GCCTTGTCCT CTTGTCCTGT

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URE 52F

2601 TTGCATTCA CTGGGAGCTT GCACTATTGC AGCTCCAGTT

2641 TCCTGCAGTG ATCAGGGTCC TGCAAGCAGT GGGGAAGGGG

2681 GCCAAGGTAT TGGAGGACTC CCTCCCAGCT TTGGAAGGGT

2721 CATCCGCGTG TGTGTGTGT TGTATGTGTA GACAAGCTCT

2761 CGCTCTGTCA CCCAGGCTGG AGTGCAGTGG TGCAATCATG

2801 GTTCACTGCA GTCTTGACCT TTTGGGCTCA AGTGATCCTC

2841 CCACCTCAGC CTCCTGAGTA GCTGGGACCA TAGGCTCACA

2881 ACACCACACC T

FIGURE 53A

	1	Chehodooc demochded Amandeded Addamand
	41	site 80 AAAGAUCAGU UAAGUCCUUU GGACCUGAUC AGCUUGAUAC
	81	site 120 AAGAACUACU GAUUUCAACU UCUUUGGCUU AAUUCUCUCG
	121	GAAACGAUGA AAUAUACAAG UUAUAUCUUG GCUUUUCAGC
	161	UCUGCAUCGU UUUGGGUUCU CUUGGCUGUU ACUGCCAGGA
	201	site 210 CCCAUAUGUA CAAGAAGCAG AAAACCUUAA GAAAUAUUU <u>U</u>
	241	site 240 site 260 AAUGCAGGUC AUUCAGAUGU AGCGGAUAAU GGAACUCUUU
;	281	UCUUAGGCAU UUUGAAGAAU UGGAAAGAGG AGAGUGACAG
	321	site 330 AAAAAUAAUG CAGAGCCAAA UUGUCUCCUU UUACUUCAAA
	361	site 380 site 400 CUUU <u>UUAAAA A</u> CUU <u>UAAAGA UGACCAGAGC</u> AUC CAAAAG A
	401	GUGUGGAGAC CAUCAAGGAA GACAUGAAUG UCAAGUUUUU
	441	CAAUAGCAAC AAAAAGAAAC GAGAUGACUU CGAAAAGCUG

ти 53В

	481	ACUAAUUAUU CGGUAACU	GA CUUGAAUGUC CAACGCAAAG	
	521	CAAUACAUGA ACUCAUCCA	site 560 AA GUGAUGGCU <u>G AACUGUCGCC</u>)
	561		e 570 GC GAAAAAG GAG UCAGAUGCUG	
	701	ARBURAN ACAGORA	GC GAAAAAGGAG UCAGAUGCUG	
	601	UUUCGAGGUC GAAGAGCA	UC CCAGUAAUGG UUGUCCUGCC	
	641	UACAAUAUUU GAAUUUUA	AA UCUAAAUCUA UUUAUUAAUA	
1 1	681	UUUAACAUUA UUUAUAUG	GG GAAUAUAUUU UUA <u>GACUC</u> AU	
	721	CAAUCAAAUA AGUAUUUA	UA AUAGCAACUU UUGUGUAAUG	
F Un 2	761	AAAAUGAAUA UCUAUUAA	LUA ÜAUGUAUUAU UUAUAAUUCC	
	801	UAUAUCCUGU GACUGUCU	JCA CUUAAUCCUU UGUUUUCUGA	. *-
5	841	site 850 CUAAUUAG GC AA GGCUAU	site 860 site JGU GAUU ACAA GG CU <u>UUAUCUCA</u>	
	881	site 890 <u>GGG</u> GCCAACU AGGCAGCC	site 910 CAA C <u>CUAAGCAAG AUCCCAUG</u> GG	
	921	. UUGUGUGUUU AUUUCACI	UUG AUGAUACAAU GAACACUUAU	ſ
	961	AAGUGAAGUG AUACUAU	CCA GUUACUA	







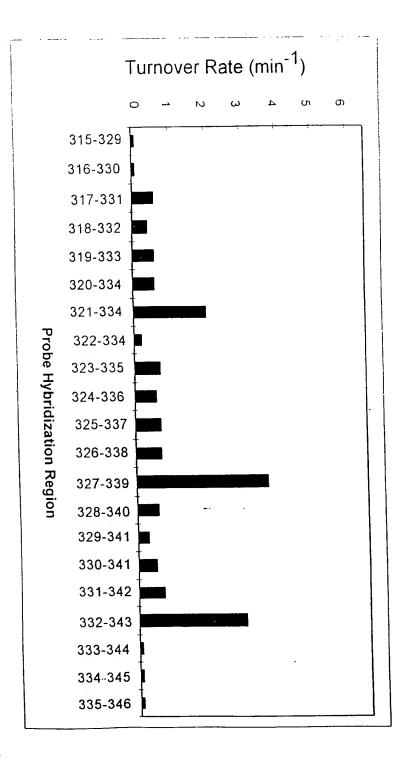


FIGURE 55A

SEQ ID NO:158

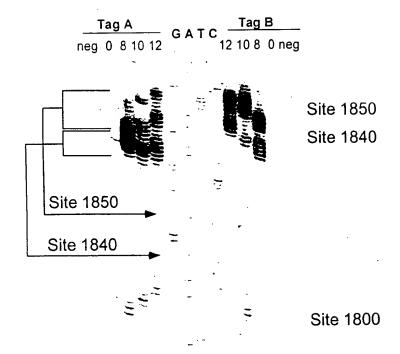
Primer 1 460 GGUCUCUCUG GUULGLCCAG AUCUGAGCCU GGGAGCUCUC UGGCUAACUA 510 GGGAACCCAC UGCUUAAGCC UCAAUAAAGC UUGCCUUGAG UGCUUCAAGU 560 AGUGUGUCC CGUCUGUUGU GUGACUCUGG UAACUAGAGA UCCCUCAGAC Primer 2 610 CCUUUUAGUC AGUGUGGAAA AUCUCUAGCA GUGGCGCCCG AACAGGGACC 660 UGAAAGCGAA AGGGAAACCA GAGGAGCUCU CUCGACGCAG GACUCGGCUU 710 GCUGAAGCGC GCACGGCAAG AGGCGAGGGG CGGCGACUGG UGAGUACGCC 760 AAAAAUUUUG ACUAGCGGAG GCUAGAAGGA GAGAGAUGGG UGCGAGAGCG Primer 3 810 UCAGUAUUAA GCGGGGGAGA AUUAGAUCGA UGGGAAAAAA UUCGGUUAAG 860 GCCAGGGGGA AAGAAAAAU AUAAAUUAAA ACAUAUAGUA UGGGCAAGCA 910 GGGAGCUAGA ACGAUUCGCA GUUAAUCCUG GCCUGUUAGA AACAUCAGAA 960 GGCUGUAGAC AAAUACUGGG ACAGCUACAA CCAUCCCUUC AGACAGGAUC Primer 4 1010 AGAAGAACUU AGAUCAUUAU AUAAUACAGU AGCAACCCUC UAUUGUGUGC 1060 AUCAAAGGAU AGAGAUAAAA GACACCAAGG AAGCUUUAGA CAAGAUAGAG

FIGURE 55B

1110 GAAGAGCAAA ACAALAGUAA GAAAAAAGCA CAGCAAGCAG CAGCUGACAC 1160 AGGACACAGC AAUCAGGUCA GCCAAAAUUA CCCUAUAGUG CAGAACAUCC Primer 5 1210 AGGGGCAAAU GGUACAUCAG GCCAUAUCAC CUAGAACUUU AAAUGCAUGG 1260 GUAAAAGUAG UAGAAGAGAA GGCUUUCAGC CCAGAAGUGA UACCCAUGUU 1310 UUCAGCAUUA UCAGAAGGAG CCACCCCACA AGAUUUAAAC ACCAUGCUAA 1360 ACACAGUGGG GGGACAUCAA GCAGCCAUGC AAAUGUUAAA AGAGACCAUC Primer 6 1410 AAUGAGGAAG CUGCAGAAUG GGAUAGAGUG CAUCCAGUGC AUGCAGGGCC 1460 UAUUGCACCA GGCCAGAUGA GAGAACCAAG GGGAAGUGAC AUAGCAGGAA 1510 CUACUAGUAC CCUUCAGGAA CAAAUAGGAU GGAUGACAAA UAAUCCACCU 1560 AUCCCAGUAG GAGAAAUUUA UAAAAGAUGG AUAAUCCUGG GAUUAAAUAA Primer 7 1610 AAUAGUAAGA AUGUAUAGCC CUACCAGCAU UCUGGACAUA AGACAAGGAC 1660 CAAAGGAACC CUUUAGAGAC UAUGUAGACC GGUUCUAUAA AACUCUAAGA 1710 GCCGAGCAAG CUUCACAGGA GGUAAAAAAU UGGAUGACAG AAACCUUGUU

FIGURE 55C

Primer 8
1810 CAGCGCUAC ACUAGAAGAA AUGAUGACAG CAUGUCAGGG AGUAGGAGAAAAA
1860 CCCGGCCAUA AGGCAAGAGU UUUGGCUGAA GCAAUGAGCC AAGUAACAAA
1910 UUCAGCUACC AUAAUGAUGC AGAGAGGCAA UUUUAGGAAC CAAAGAAAGA
1960 UUGUUAAGUG UUUCAAUUGU GGCAAAGAAG GGCACACAGC CAGAAAUUGC
2010 AGGGCCCCUA GGAAAAAGGG CUGUUGGAAA UGUGGAAAGG AAGGACACCA
2060 AAUGAAAGAU UGUACUGAGA G

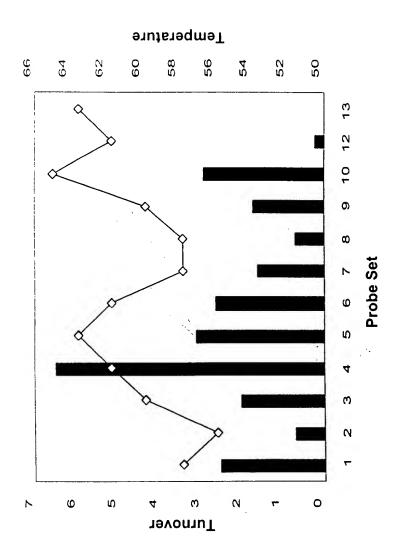


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FIGURE 57

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	:. O Z	
11	OII.	
13 12 10=1. 9 8 7 7 6 6 6	2 1 1.AG-3 (SEQ	
ر ر	AAUG	
rgcri	AGC	
AACT AACT AACT	20GA 664) 665) 667) 771) 773) 755)	
00004 00004 00004 00004 00004	2 JUUGGCUGAAGCAAUGAG-3 NO:164) (SEQ NO:166) NO:166) NO:168) NO:169) NO:170) NO:171) NO:172) NO:173) NO:174)	
CGTATTCCGTTCTCAAAACCGACTTGCT-5' AGGTATTCCGTTCTCAAAACCGACT ACGGTATTCCGTTCTCAAAACCGAC CCCGGTATTCCGTTCTCAAAACCGA CGCCGGTATTCCGTTCTCAAAACCG AGGCCGGTATTCCGTTCTCAAAACCAAACC	a 5888888888888	
CGTATTCCGTTCTCAAA AGGTATTCCGTTCTCAAA ACGGTATTCCGTTCTCAAA CCCCGGTATTCCGTTCTCAAA CGCCGGTATTCCGTTCTCAAA AGGCCGGTATTCCGTTCTCAAA AGGCCGGTATTCCGTTCTCAAA ATGGCCGGTATTCCGTTCTCAAA ACTGGCCGGTATTCCGTTCTCAAA	ATCCTGGCCGGTATTCCGTTCTCA ACTCCTGGGCCGGTATTCCGTTCTC GGAGGACCCGCCAUAAGGCAAGAGG CCT CCT CCT CCTC CCTCC CCTCCT CCTCCT CCTCCT CCTCCT CCTCCTGGC CCTCCTGGC CCTCCTGGC CCTCCTGGC CCTCCTGGC CCTCCTGGC CCTCCTGGC CCTCCTGGC CCTCCTGGC CCTCCTGGC CCTCCTGGC CCTCCTGGC CCTCCTGGCC CCTCCTGGCC CCTCCTGGCC CCTCCTGGGC CCTCCTGGCC CCTCCTGGCC CCTCCTGGCC CCTCCTGGCC CCTCCTGGCC CSEQ I CCTCCTGGCC CCTCCTGGCC CCTCCTGGCC CCTCCTGGCC CCTCCTGGCC CCTCCTGGCC CCTCCTGGCC CCTCCTGGCC CCTCCTGGCCC CCTCCTGGCCC CCTCCTGGCCCCAAAAAA-FLC-5,	
		,
CGTATTCC AGGTATTCC ACGGTATTCC CCCCGGTATTCC CGCCCGGTATTCC AGGCCCGGTATTCC ACTGGCCCGGTATTCC ACTGGCCCGGTATTCC	A-F1	
0617 0617 0617 0617 0617	SGTP	
	ATCCTGGGCCG CTCCTGGGCCG GAGGACCCGGC CTC CTC CTCCTGG CTCCTGGG CTCCTGGGC CTCCTGGGC CTCCTGGGC	
CG CG AGG CTGG CTGGG	ATCCTGGGCC ACTCTGGGGC ATCC ATCCT ATCCTC ATCCTC ATCCTCC ATCCTCT ATCCTCTGG ATCCTCTGG ATCCTCTGGC CTCCTGGGC CTCCTGGGC CTCCTGGGC CTCCTGGGC	
ACC		
888) 887) 885) 882) 79)	HITAN ALTCOT AGGGAGUAGGAGGA TCCCTCATCC TCCCTCATCC TCCCTCATCCT TCCCTCATCCT TCCTCATCCT TCCTCATCCT TCCTCATCCTC TCCTCATCCTC TCCTCATCCTC TCATCCTCCT TCATCCTCCT TCATCCTCCT TCATCCTCCT TCATCCTCCT ATCTCCTCTCC	
NOO: 1887 NOO: 1887 NOO: 1886 NOO: 1887 NOO: 1818 NOO: 1818 NOO: 1818 NOO: 1798	NO: 178) ATCCTGGGCCGGTATTCCGTTCTC NO: 177) ACTCCTGGGCCGGTATTCCGTTCTC SUCAGGGAGUAGGAGGACCCGGCCAUAAGGCAAGAG SAGTCCTCATCT CTCCTCATCCT CCCTCATCCTC CCTCATCCTC CCTCATCCTC CCTCATCCTCC CTCATCCTCG CTCATCCTCGG ATCCTCCTGGG ATCCTCCTGGGC CSEQ CTCATCCTCGGGC CSEQ CTCATCCTCGGGC CSEQ CTCATCCTCGGGC CSEQ CTCATCCTCGGGC CSEQ CSEQ CTCATCCTCGGGC CSEQ CSEQ CSEQ CTCCTCGGGC CSEQ CTCCTCGGGC CSEQ CTCCTCGGGCC CSEQ CTCCTCGGGCC CSEQ CTCCTCGGGCCCGA _{AAA} -FL-5,	
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FIGURE 59

(SEQ ID NO:180)

ACTGGGCCGGTATTCCGTTCTAAA 5'-CAUGUQ<u>AGGG</u>AGUAGGACCCGGCCAUAAGGCAAGAGUUUUGGCUGAAGCAAUGAG-3'

(SEQ ID NO:189)

TCCCTCATCCTCCTCCGCACTGCC-5,

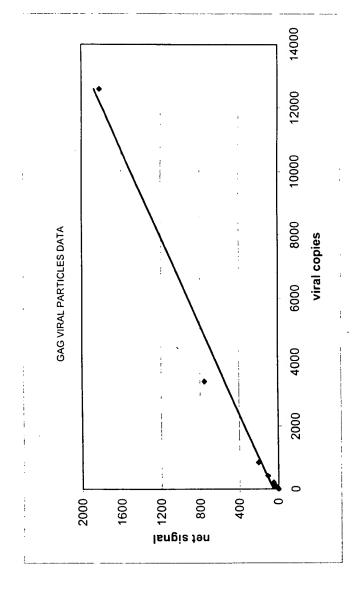
5'-AGGGAGTAGGAGGAGG-3'

(SEQ ID NO:190)

(SEQ ID NO:193) CAAC GCTTCCTCCG-3' Ø <u>→</u> Ø

5'- CCGTCACGCCTCC
3'-TGGCAGTGCGGAGGAGAGAGGC-5' (SEQ ID NO:191)

(SEQ ID NO:192)



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FIGURE 61A

SEQ ID NO:159

	primer 1			
3300	AGCUGGACUG UCAAUGA	CAU ACAGAA GUU	GUGG GGAAAU	UG AAUUG GGC
3350	AAGUCAGAUU U ACCCA G	:GGA UUA AAGUAA	GCAAUUAUGU	AAACUCCUUA
3400	GAGGAACCAA AGCACUA	ACA GAAGUAAUAC	CACUAACAGA	AGAAGCAGAG
3450	CUAGAA CUG G CAGAAAA	ACAG AGAGAUUCUA	A AAAGAACCAG	UACAUGGAGU
3500	primer 2 GUAUUAUGAC CCAUCAP	AAAG ACUUAAUAGG	AGAAAU ACAG	AAGCAGGGGC
3550	AAGGCCAAUG GACAUAL	JCAA AUUUAU CAA	G AGCCAUUUAA	AAAUCUGAAA
3600	ACAGGAAAAU AUGCAAC	GAAU GAGG GGUGC	C CACACUAAUG	AUGUAAAACA
3650	AUUAACA GAG G CAGUGO	CAAA AAAUAACCA	C AGAAAGCAUA	GUAAUAUĢGG
3700	primer 3 GAAAGACUCC UAAAUUU	JA AA CU GCCCAUA	C AAAAGGAAAC	AUGGGAAACA
3750	UGGUGGACAG AGUAUU	GGCA AGCCACCUG	G AUUCCUGAGU	GGGAGUUUGU
3800	UAAUACCCCU CCCUUA	GUGA AAUUA UG GU	A CCAGUUAGAG	AAAGAACCCA
3850	UAGU AGG AGC AGAAAC	CUUC UAUGUAGAU	G GG GCAGCUAA	A CAGG GAGACU
3900	primer 4 AAAUUAGGAA AAGCAG	GAUA UGUUACUAA	, U AGAG GAAGAO	C AAAAAGUUGU

FIGURE 61B

3950	CACCCUAACU	GACACAACAA	AUCAGAAGAC	UGAGUUACAA	GCAAUUUAUC
4000	UAGCUUUGCA	GGAUU CGG GA	UUAGAAGUAA	ACAUAGUAAC	AGACUCACAA
4050	UAUGCAUUAG	GAAUCAUUCA	AGCACAA CCA	GAUCAAAGUG	AAUCAGAGUU
4100	primer S AGUCAAUCAA		<u>AG</u> UUAAUAAA	AAAGGAAAAG	GUCUAUC UGG
4150	C AUGGGUACC	AGCACACAAA	GGA AUUGGAG	GAAAUGAACA	AGUAGAUAAA
4200	UUAGUCAGUG	CUGGAAUCAG	GAAAGUACUA	UUUUUAGAUG	GAAUAGA UAA
4250	GGC CCAAGAU	GAACAUGAGA	AAUAUCACAG	UAAUU GGAG A	GCAAUGGCUA
4300	primer 6 GUGAUUUUAA		GUAGUAGCAA	AAGAAAUA GU	AGC CAGCUGU
4350	GAUAAAUGUC	AGCUAAAAGG	AGAAGCCAUG	CAUGGACAAG	UAGACUGUAG
4400	UCCAGGAAUA	UGGCAACUAG	AUUGUACACA	UUUAGAAGGA	AAAGUUAUCC
4450	UGGUAGCAGU	UCAUGUAGCC	AGUGGAUAUA	UA GAA GCAGA	AGUUAUUCCA
4500	primer GCAGAAACAG		AGCAUAUUUU	CUUUUAAAAU	UAGCAGGAAG
4550	AUGG CCAGUA	AAAACAAUAC	AUA CUGACAA	UGG CAGCAAU	UUC ACCGG UG
4600	CUACGGUUAG	GGCCGCCUGU	UGGUGGGCGG	GAAUCA AGCA	G GAAUUUGGA

FIGURE 61C

4630	AUUCCCOACA	AUCCCCAAAG	OCAMOUN.	00/10/2100011	00.2.0.2.0
4700	primer 8 AUUAAAGAAA		AGG UAAGAGA	UCAGG CUGAA	CAUCUUAAGA
4750	CAGCAGUACA	AAUGGCAGUA	UUCAUCCACA	AUUUUAAAAG	AAA AGGG GGG
4800	AUUGGGGGGU	AC AGUGCAGG	GGA AAGAAUA	GUAGACAUAA	UAGCAACAGA
4850	CAUACAAACU	AAAGAAUUAC	AAAAACAAAU	UACAAAAAUU	CAAAAUUUUC
4900	primer S GGGUUUAUUA		AGAAAUCCAC	UUUGGA AAGG	ACCAGCAAAG
4950	CUCCUCUGGA	AAGGUG AAGG	GGCAGUAGUA	AUACAAGAUA	AUAGUGACAU
5000	AAAA GUAGU G	CCAAGAAGAA	AAGCAAAGAU	CAUUAGGGAU	UAUGGAAAAC
5050	AGAUGGCAGG	UGAUGAUUGU	G		

FIGURE 62

CTCGTCTTTAGGTGAAACCTTTCCT-5'2 AGTCGTCTTTAGGTGAAACCTTTCCT-5 · 1 ATGTTTTAAGTTTTAAAAGC 3'-CTGTATGTTTGATTTCTTAATGTTTTTGTTTA 5'-GACAUACAAACUAAAGAAUUACAAAAACAAAU (SEQ ID NO:159) (SEQ ID NO:198)

(SEQ ID NO:197)

(SEQ ID NO:196)

(SEQ ID NO:203)
33'-AGCCCAAATAATGTCCCTGTCGTC (SEQ ID NO:204)

ACTGGTCGTTTCGAGGAGACC-5'3 (SEQ ID NO:201)

4910

(SEQ ID NO:202)

(SEQ ID NO:159)

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FIGURE 63

(SEQ ID NO:203) ACCCGTCATTATGTTCTATTATCACGTTTT-5: 5 6 3'-CCTGGTCGTTTCAGGAGA 5'-CCTGGTCGTTTCAGGAGAC 5'-GAAAGGACCAGCAAAGGUQAAGGUGAGGSCAGUAGUAAUACAAGAUAAUAGUAAUAGUAGUSC-3' 6 CTTCCACTTCCAAAGGUQAAGGUAAAGGUQAAAGGUAGAGGACAAAAGGUAGAAAGGUAAAAGGUAAAAGGUAAAAGGUAAAAGGUAAAAAGGUAAAAAGGUAAAAAGGUAAAAAA	(SEQ ID NO:215) (SEQ ID NO:211) (SEQ ID NO:212) (SEQ ID NO:159) (SEQ ID NO:208) 4960 (SEQ ID NO:208)
5 3'-TCCTGGTCGTTCGAGGAGA 6 3'-CCTGGTCGTTTCGAGGAGC 5'-GA <u>AAGG</u> ACCAGCAAAGCUCCUCGGAAAGGUGAA 4930 6 CTTTCCACTT 4930 4930 5 CCTTTCCACTT 4930	(SEQ ID NO:215) 73'-TCGAGGAGACCTTTCCAC (SEQ ID NO:216) 83'-TCGAGGAGACCTTTCCACT 5'-GAAAGGACCAAAGCUCCUCUGGAAAGGUGAAGGGG 4930 7 TTCCC 4950

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FIGURE 64

(SEQ ID NO:221) TCACGTCCCCAAAAS, (SEQ ID NO:217) 4810 (SEQ ID NO:224)

5 - AGACAGCAGUACAAAUGGCAGUAUUCAUCCACAAUUUUAAAAGAAA<mark>AGGG</mark>SGGAUUGGGGGGGUAC<mark>AGUGCAGGGGA</mark>AAG-3 (SEQ ID NO:159) ACCCTAACCCCCCATGTCAC-5' GTTAAAATTTTCTTTTCCCAAAAAS (SEQ ID NO:220) (SEQ ID NO:222) 4790 3'-CTGTCGTCATGTTTACCGTCATAAGTAGGT (SEQ ID NO:225)

4810 (SEQ ID NO:222) 4790

က

(SEQ ID NO:223)

CATCATCTGTATTATCGTTGTCTGTATGTTTGATTTC ACCCTAACCCCCCATGTCAC-5'

5 - <u>- aayaggg</u>gggauugggggguad<u>agugcaggggab</u>agaauaguagacauaauagcaacaacagacauacaaacuaaagaa-3 (SEQ ID NO:159) GTCCCCTTTCTTA_{dad}, (SEQ ID NO:219)

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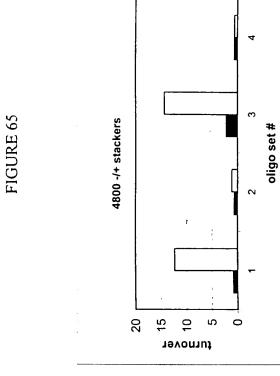


FIGURE 66

4790

4810

(SEQ ID NO:221)

(SEQ ID NO:224)

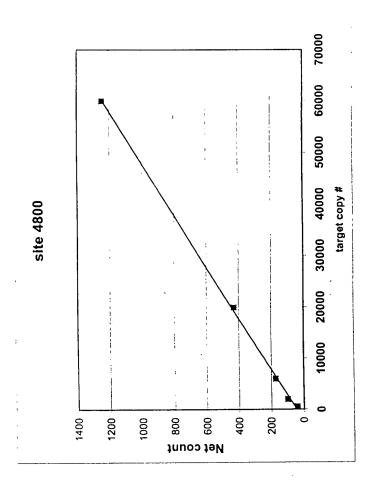
5'-AGTGCAGGGGGGGGGG-3' (SEQ ID NO:227)

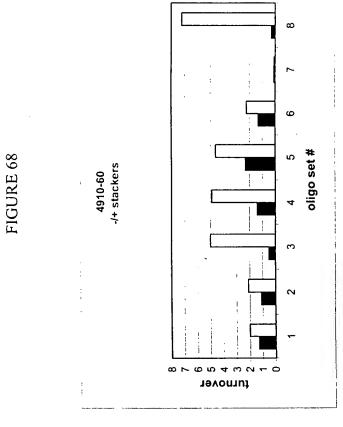
(SEQ ID NO:193) (SEQ ID NO:191)

5'- CCGTCACGCCTCC

E W (SEQ 12 CAAC GCTTCCTCCG-3' 3'-TGGCAGTGCGGAGGTTGACGAAGAGGC-5' (SEQ ID NO:192)

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FIGURE 69

4960 (SEQ ID NO:213)

5:-GARAGGACCAGCAAAGCUCCUCGGAAAGGUGBAGGGCCAGUAGUAAUACAAGAUAAUAGUGACAUAAAAGUBC-3:

(SEQ ID NO:159)

4930 (SEQ ID NO:228) ACCCGTCATCATTATGTTCTATTATCACTGTATTTT-5' 3'-TCCTGGTCGTTTCGAGGAGA

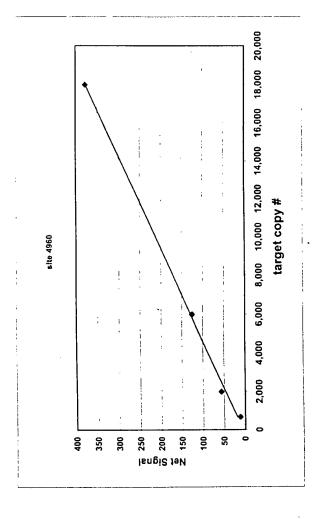
(SEQ ID NO:209)

(SEQ ID NO:193)

(SEQ ID NO:191)

5'-GGAAAGGTGAAGGAGGC-3' (SEQ ID NO:229)

5'- CCGTCACGCCTCC
3'-TGGCAGTGCGGAGGTTGACGAAGAAGGC-5'
(SEQ ID NO:192)



Human PSP94

383-31-1	5'-TET-CCTGCTTATCACAATGAA-3'	(SEQ	ID	NO:230)
383-31-3	5'-TET-ACATGCACTTGCTACGAAAC-3'	(SEQ	ID	NO:231)

SEQ ID NO:232

Human ubiquitin:

520-77-1 5'-TET-CCGCCACCAAAATGC-3' (SEQ ID NO:233) 520-59-2 5'-TET-GCTGGAAGATGGACG-3' (SEQ ID NO:234)

SEQ ID NO:235

CCGCCACCAAAAUGCAGAUUUUCGUGAAAACCCUUACGGGGAAGACCAUCACCCUCGAG
GUUGAACCCUCGGAUACGAUAGAAAAUGUAAAGGCCAAGAUCCAGGAUAAGGAAGAAU
UCCUCCUGACAGCAGAGACUGAUCUUUGCUGGCAAGCAGCUGGAAGAUGGACGUACUUUG
UCUGACUACAAUAUUCAAAAGGAGUCUACUCUUCAUCUUGUUUGAGACUUCGUGGUGG
UGCUAAGAAAAGGAAGAAGAAGUCUUACACCACUCCCAAGAAGAAUAAGCACAAGAGAAA
GAAGGUUAAGCUGGCUGUCCUGAAAUAUUAUAAGGUGGAUGAGAAUGGCAAAAUUAGUC
GCCUUCGUCGAGAGUGCCCUUCUGAUGAUGAUGGUGGUGCUGGGGUGUUUAUGGCAAGUCACU

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FIGURE 73

HCV-la 5'-UTR:

898-28-01	5'-TET-GGGACACTCCACCATGAATCACTC-3'	(SEQ	ID	NO:236)
898-35-01	5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3'	(SEQ	ID	NO:237)
898-35-02	5'-TET-ATTTGGGCGTGCCCCGC-3'	(SEQ	ID	NO:238)
898-35-03	5'-TET-GACCGGGTCCTTTCTTGGA-3'	(SEQ	ID	NO:239)

SEQ ID NO:240

GGGACACUCCACCAUGAAUCACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAUGAGUGUCGUGCAGCCUCCAGGACCCCCCCUCCCGGGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUUGCCAGGACGACCGGGUCCUUUC
UUGGAUAAACCCGCUCAAUGCCUGGAGAUUUGGGCGUCCCCCCCAAGACUGCUAGCCG
AGUAGUGUUGGGUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCC
CCGGGAGGUCUCGUAGACCGUGCACCAUGAG

HCV-1b 5'-UTR:

898-28-02	5'-TET-GGGACACTCCACCATAGATCACTC-3'	(SEQ	ID	NO:241)
898-35-01	5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3'	(SEQ	ID	NO:237)
898-35-02	5'-TET-ATTTGGGCGTGCCCCGC-3'	(SEQ	ID	NO:238)
898-35-03	5'-TET-GACCGGGTCCTTTCTTGGA-3'	(SEQ	ID	NO:239)

SEQ ID NO:242

GGGACACUCCACCAUAGAUCACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAGAACGGUGAGUACACCGGAAUUGCCAGGACCCCCCUUCCCGGGAGAGG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUUGCCAGGACGACCGGGUCCUUUC
UUGGAUCAACCCGCUCAAUGCCUGGAGAUUUGGGCGUGCCCCCCCGCGAGACUGCUAGCCG
AGUAGUGUUGGGUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUĢCGAGUGCC
CCGGGAGGUCUCGUAGACCGUGCACCAUGAG

FIGURE 75

HCV 2a/c 5'-UTR:

898-28-01 5'-TET-GGGACACTCCACCATGAATCACTC-3'(SEQ ID NO:236) 898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3'(SEQ ID NO:237) 898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238) 898-35-03 5'-TET-GACCGGGTCCTTTCTTGGA-3' (SEQ ID NO:239)

SEQ ID NO:243

GGGACACUCCACCAUGAAUCACUCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAUGAGUGUCGUACAGCCUCCAGGCCCCCCCUCCCGGGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUUGCCGGGAAGACUGGGUCCUUUC
UUGGAUAAACCCACUCUAUGCCCGGCCAUUUGGGCGUGCCCCCGCAAGACUGCUAGCCGA
GUAGCGUUGGGUUGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCCCC
GGGAGGUCUCGUAGACCGUGCACCAUGAG

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FIGURE 76

HCV 3a 5'-UTR:

898-28-03	5'-TET-GGGACACTCCACCATGGATCACTC-3'	(SEQ	ID	NO:244)
898-35-01	5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3'	(SEQ	ID	NO:237)
898-35-02	5'-TET-ATTTGGGCGTGCCCCGC-3'	(SEQ	ID	NO:238)
898-35-03	5'-TET-GACCGGGTCCTTTCTTGGA-3'	(SEO	TD	NO-2391

SEQ ID NO:245

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FIGURE 77A

Human Antigen CD36 mRNA Oligonucleotides

726-38-01	5 '-ACAAGGGAAGAGAGATGAGGAACCAG-3 '	(SEQ	TD	NO:246)
666-33-01	5'-TTTGCCTTCTCATCACCAATGG-3'	(SEQ	ID	NO:247)
937-03-01	5'-TET- aagggaagagatgag-3'	(SEQ	ID	NO:248)
937-03-02	5'-TET-aggagtttgcaagaaac-3'	(SEQ	ID	NO:249)
937-03-03	5'-TET-ggtgctgtcctgg-3'	(SEQ	ID	NO:250)
937-03-04	5'-TET-cagttttggatctttgatg-3'	(SEQ	ID	NO:251)
937-03-05	5'-TET-aggacgctgagga-3'	(SEQ	ID	NO:252)
937-03-06	5'-TET-aacaagtcaaaatcttctatg-3'	(SEQ	ID	NO:253)
937-03-07	5'-TET-caatactgcagatggag-3'	(SEQ	ID	NO:254)
937-03-08	5'-TET-aagccaggtattgca-3'	(SEQ	ID	NO:255)
937-03-09	5'-TET-ctattgtttctgcacaga-3'	(SEQ	ID	NO:256)
937-03-10	5'-TET-aaatgaagaagaacatagga-3'	(SEQ	ID	NO:257)
937-03-11	5'-TET-ggtcaagccatcaga-3'	(SEQ	ΊD	NO:258)

FIGURE 77B

Human Antigen CD36 mRNA (SEQ ID NO:259)

ACAAGGGAAGAGAGAUGAGGAACCAGAGCUUGUAGAAACCACUUUAAUCAUAUCCAGGA GUUUGCAAGAAACAGGUGCUUAACACUAAUUCACCUCCUGAACAAGAAAAAUGGGCUGU GACCGGAACUGUCGGCUCAUCGCUCGGCUGUCAUUGGUGCUGUCCUGGCUGUGUUUGG AGGUAUUCUAAUGCCAGUUGGAGACCUGCUUAUCCAGAAGACAAUUAAAAAGCAAGUUG UCCUCGAAGAAGUACAAUUGCUUUUAAAAAUUGGGUUAAAACAGGCACAGAAGUUUAC AGACAGUUUUGGAUCUUUGAUGUGCAAAAUCCACAGGAAGUGAUGAUGAACAGCAGCAA CAUUCAAGUUAAGCAA\AGAGGUCCUUAUACGUACAGAGUUCGUUUUCUAGCCAAGGAAA AUGUAACCCAGGACGCUGAGGACAACACAGUCUCUUUCCUGCAGCCCAAUGGUGCCAUC UUCGAACCUUCACUAUCAGUUGGAACAGAGGCUGACAACUUCACAGUUCUCAAUCUGGC UGUGGCAGCUGCAUCCCAUAUCUAUCAAAAUCAAUUUGUUCAAAUGAUCCUCAAUUCAC UUAUUAACAAGUCAAAAUCUUCUAUGUUCCAAGUCAGAACUUUGAGAGAACUGUUAUGG GGCUAUAGGGAUCCAUUUUUGAGUUUGGUUCCGUACCCUGUUACUACAGUUGGUCUG UUUUAUCCUUACAACA LUACUGCAGAUGGAGUUUAUAAAGUUUU CAAUGGAAAAGAUAA CAUAAGUAAAGGUUGCCAUAAUCGACACAUAUAAAGGUAAAAGGAAUCUGUCCUAUUGGG AAAGUCACUGCGACAUGAUUAAUGGUACAGAUGCAGCCUCAUUUCCACCUUUUGUUGAG AAAAGCCAGGUAUUGCAGUUCUUUUCUGAUAUUUGCAGGUCAAUCUAUGCUGUAUU CCUUUGCCUCUCCAGUUGAAAACCCAGACAACUAUUGUUUCUGCACAGAAAAAUUAUC UCAAAAAUUGUACAUCAUAUGGUGUGCUAGACAUCAGCAAAUGCAAAGAAGGAGACC UGUGUACAUUUCACUUCCUCAUUUUCUGUAUGCAAGUCCUGAUGUUUCAGAACCUAUUGA UGGAUUAAACCCAAAUGAAGAAGAACAUAGGACAUACUUGGAUAUUCAACCUAUAA<mark>CU</mark>G GAUUCACUUUACAAUUUGCAAAACGGCUGCAGGUCAACCUAUUGGUCAAGCCAUCAGAA AAAAUUCAAGUAUUAAAGAAUCUGAAGAGGAACUAUAUUGUGCCUAUUCUUUGGCUUAA UGAGACUGGGACCAUUGGUGAUGAGAAGGCAAA

FIGURE 78

Human Ribosomal Protein L5 mRNA

761-47-01	5'-ATGGGGTTTGTTAAAGTTG-3'	(SEQ	ID	NO:260)
761-47-02	5'-GCTGGGTTTAGCTCTCAGCAGCCCGC-3'	(SEQ	ID	NO:261)
937-05-01	5'-TET- atggggtttgttaaagtt-3'	(SEQ	ID	NO:262)
937-05-02	5'-TET- gaagacgacgagagg-3'	(SEQ	ID	NO:263)
937-05-03	5'-TET- ggatgatagttcgtgtg-3'	(SEQ	ID	NO:264)
937-05-04	5'-TET- gctgcagcatattgta-3'	(SEQ	ID	NO:265)
937-05-05	5'-TET- ctgctatttggatgca-3'	(SEQ	ID	NO:266)
937-05-06	5'-TET- gcagaagtacatcgga-3'	(SEQ	ID	NO:267)
937-05-07	5'-TET- gacatgatggaggaga-3'	(SEQ	ID	NO:268)
937-05-08	5'-TET- agaagaaggatcggg-3'	(SEQ	ID	NO:269)

SEQ ID NO:270

AUGGGGUUUGUUAAAGUUGUUAAGAAUAAGGCCUACUUUAAGAGAUACCAAGUGAAAUU UAGAAGACGACGAGAGGGUAAAACUGAUUAUUAUGCUCGGAAACGCUUGGUGAUACAAG AUAAAAUAAAUACEACACCCAAAUACAGGAUGAUAGUUCGUGUGACAAACAGAGAU AUCAUUUGUCAGAUUGCUUAUGCCCGUAUAGAGGGGGAUAUGAUAGUCUGCGCACGUUA UGCACACGAACUGCCAAAAUAUGGUGUGAAGGUUGGCCUGACAAAUUAUGCUGCAGCAU AUUGUACUGGCCUGCUGGCCCGCAGGCUUCUCAAUAGGUUUGGCAUGGACAAGAUC UAUGAAGGCCAAGUGGAGGUGACUGGUGAUGAAUACAAUGUGGAAAGCAUUGAUGGUCAG CCAGGUGCCUUCACCUGCUAUUUGGAUGCAGGCCUUGCCAGAACUACCACUGGCAAUAA AGUUJUUUGGUGCCUGAAGGGAGCUGUGGAUGGAGGCUUGUCUAUCCCUCACAGUACCA AACGAUUCCCUGGUUAUGAUUCUGAAAGCAAGGAAUUUAAUGCAGAAGUACAUCGGAAG CACAUCAUGGCCAGAAUGUUGCAGAUUACAUGCGCUACUUAAUGGAAGAAGAUGAAGA UGCUUACAAGAAACAGUUCUCUCAAUACAUAAAGAACAGCGUAACUCCAGACAUGAUGG AGGAGAUGUAUAAGAAAGCUCAUGCUGCUAUACGAGAGAAUCCAGUCUAUGAAAAGAAG CCCAAGAAAGAAGUUAAAAAGAAGAGGUGGAACCGUCCCAAAAUGUCCCUUGCUCAGAA GAAGGAUCGGGUAGCUCAAAAGAAGGCAAGCUUCCUCAGAGCUCAGGAGCGGGCUGCUG AGAGCUAAACCCAGC

FIGURE 79A

Mouse Scavenger Receptor Class B Type I mRNA Oligonucleotides

726-39-01	5'-GCTCA	AGAATGTCCGCATAGACCCG-3'	(SEQ	ID	NO:271)
666-34-01	5'-CTGGT	CCCTGAGTTGTTTTTGC-3 '	(SEQ	ID	NO:272)
937-01-01	5'-TET-	GCTCAAGAATGTCCG-3'	(SEQ	ID	NO:273)
937-01-02	5'-TET-	gggatgtggaaggag-3'	(SEQ	ID	NO:274)
937-01-03	5'-TET-	ggaccctatgtctacag-3'	(SEQ	ID	NO:275)
937-01-04	5'-TET-	acatettggteetgg-3'	(SEQ	ID	NO:276)
937-01-05	5'-TET-	tctcaacacgtacctc-3'	(SEQ	ID	NO:277)
937-01-06	5'-TET-	cggactcagcaaga-3'	(SEQ	ID	NO:278)
937-01-07	5'-TET-	caagggtgtttgaagg-3'	(SEQ	ID	NO:279)
937-01-08	5'-TET-	ctctgtttctctccca-3'	(SEQ	ID	NO:280)
937-01-09	5'-TET-	gtgaagatgcagctg-3'	(SEQ	ID	NO:281)
937-01-10	5'-TET-	agctggtgctgatg-3'	(SEQ	ÍD	NO:282)
937-01-11	5'-TET-	caggcctactctgag-3'	(SEQ	ID	NO:283)
937-01-12	5'-TET-	ggactctctcagcg-3'	(SEQ	ID	NO:284)

FIGURE 79B

Mouse Scavenger Receptor Class B Type I mRNA (SEQ ID NO:285)

GCUCAAGAAUGUCCGCAUAGACCCGAGCAGCCUGUCCUUCGGGAUGUGGAAGGAGAUCC CCGUCCCUUUCUACUUGUCUGUCUACUUCUUCGAAGUGGUCAACCCAAACGAGGUCCUC AACGGCCAGAAGCCAGUAGUCCGGGAGCGUGGACCCUAUGUCUACAGGGGAGUUCAGACA AAAGGUCAACAUCACCUUCAAUGACAACGACACCGUGUCCUUCGUGGAGAACCGCAGCC UCCAUUUCCAGCCUGACAAGUCGCAUGGCUCAGAGAGUGACUACAUUGUACUGCCUAACA UCUUGGUCCUGGGGGCUCGAUAUUGAUGGACAAGCCUGUGAGCCUGAAGCUGAUG AUGACCUUGGCGCUGGUCACCAUGGGCCAGCGUGCUUUUAUGAACCGCACAGUUGGUGA GAUCCUGUGGGGCUAUGACGAUCCCUUCGUGCAUUUUUCUCAACACGUACCUCCCAGACAU GCUUCCCAUAAAGGGCAAAUUUGGCCUGUUUGUUGGGAUGAACAACUCGAAUUCUGGGG UCUUCACUGUCUUCACGGGCGUCCAGAAUUUCAGCAGGAUCCAUCUGGUGGACAAAUGG AACGGACUCAGCAAGAUCGAUUAUUGGCAUUCAGAGCAGUGUAACAUGAUCAAUGGGAC UUCCGGGCAGAUGUGGGCACCCUUCAUGACACCCGAAUCCUCGCUGGAAUUCUUCAGCC CGGAGGCAUGCAGGUCCAUGAAGCUGACCUACAACGAAUCAAGGGUGUUUGAAGGCAUU CCCACGUAUCGCUUCACGGCCCCGAUACUCUGUUUGCCAACGGGUCCGUCUACCCACC CAACGAAGGCUUCUGCCCAUGCCGAGAGUCUGGCAUUCAGAAUGUCAGCACCUGCAGGUU UGGUGCGCCUCUGUUUCUCCCACCCCCACUUUUAQAACGCCGACCCUGUGUUGUCAG AAGCUGUUCUUGGUCUGAACCCUAACCCAAAGGAGCAUUCCUUGUUCCUAGACAUCCAŪ CCGGUCACUGGGAUCCCCAUGAACUGUUCUGUGAAGAUGCAGCUGAGCCUCUACAUCAA AUCUGUCAAGGGCAUCGGGCAAACAGGGAAGAUCGAGCCAGUAGUUCUGCCGUUGCUGUG GUUCGAACAGAGCGGAGCAAUGGGUGGCAAGCCCCUGAGCACGUUCUACACGCAGCUGGU GCUGAUGCCCCAGGUUCUUCACUACGCGCAGUAUGUGCUGCUGGGGCCUUCGU GUUGCUGGUGCCCAUCAUCUGCCAACUGCGCAGCCAGGAGAAAUGCUUUUUUGGA GUGGUAGUAAAAAGGGCUCCCAGGAUAAGGAGGCCAUUCAGGCCUACUCUGAGUCCCUGA UGUCACCAGCUGCCAAGGCACGGUGCUGCAAGAAGCCAAGCUAUAGGGUCCUGAAGACA CUAUAAGCCCCCCAAACCUGAUAGCUUGGUCAGACCAGCCACCCAGUCCCUACACCCCG CUUCUUGAGGACUCUCUCAGCGGACAGCCCACCAGUGCCAUGGCCUGAGCCCCCAGAUGU CACACCUGUCCGCACGCACGCACGGCACGCAUGUGCAAAAACAACUCAGGGA **CCAG**

FIGURE 80A

Rat CX3CR1 Accession No. U04808 Oligonucleotides

	761-57-01 5'-taatacgactcactatagggacggaagtccaagagcatcactg-3		
			(SEQ ID NO:286)
	761-57-03	5'-gcaggtacctggtccgta-3'	(SEQ ID NO:287)
	781-65-01	5'-TET-ggaagtccaagagca-3'	(SEQ ID NO:288)
	781-65-02	5'-TET-aatggcttctttggg-3'	(SEQ ID NO:289)
	781-65-03	5'-TET-ggcgtcgccc-3'	(SEQ ID NO:290)
	781-65-04	5'-TET-tacttccgcatcgtc-3'	(SEQ ID NO:291)
	781-65-05	5'-TET-cttcttccctagttgtg-3'	(SEQ ID NO:292)
	781-65-06	5'-TET-tgcctggccgt-3'	(SEQ ID NO:293)
0	781-65-07	5'-TET-gactctactaagaaccca-3'	(SEQ ID NO:294)
ā	781-73-01	5'-TET-ccatcttagtggcgt-3'	(SEQ ID NO:295)
9= ===	781-73-02	5'-TET-caacaagtgcctgg-3'	(SEQ ID NO:296)
	781-85-01	5'-TET-aacacggcgtcac-3'	(SEQ ID NO:297)
	781-85-02	5'-TET-tgattaccccgagg-3'	(SEQ ID NO:298)
٥î	781-85-03	5'-TET-acgctgttttcctg-3'	(SEQ ID NO:299)
Ū ⊢	781-85-04	5'-TET-tgagacacctgtacaa-3'	(SEQ ID NO:300)
	781-85-05	5'-TET-gacggagacagtgg-3'	(SEQ ID NO:301)
غب	781-85-06	5'-TET-caagcgagggagag-3'	(SEQ ID NO:302)

FIGURE 80B

Rat CX3CR1 Accession No. U04808 (SEQ ID NO:303)

GGAAGUCCAAGAGCAUCACUGACAUCUACCUCCUGAACCUGGCCUUGAGCGACCUGCUC UUUGUGGCCACUUUGCCCUUCUGGACUCACUACCUCAUCAGCCAUGAGGGCCUCCACAA CGCCAUGUGCAAGCU<mark>CA</mark>CGACUGCUUUCUUCAUUGGCUUCUUU<mark>GG</mark>GGGCAUAUUCU UCAUCACGUCAUCAGCAUCGACCGGUJACCUCGCCAUCGUCCUGGCCGCCAACUCCAUG AACAACCGGACAGUGCAACACGGCGUCACCAUCAGUCUGGGCGUCUGGGCGGCCAU AUUACCCCGAGGUCCUGCAGGAAAUCUGGCCCGUGCUCCGCAACUCGGAGGUCAACAUC CUGGGCUUCGUCCUUGCUUAUCAUGAGCUUUUGCUACUUCCGCAUCGUCCGGAC GCUGUUUUCCUGCAAGAACCGGAAGAAGGCCAGAGCCAUUAGGCUCAUCCUCUUGGUGGU UGUUGUCUUCUUCUUCUGGACGCCUUACAACAUCGUGAUUUUCCUGGAGACUCUCA AAUUCUACAACUUCUUCCCUAGUUGUGGCAUGAAGAGGGGCCCUUAGU GUGACGGAGACAGUGGCGUUUAGCCACUGCUGCCUCAACCCCUUUAUCUACGCUUUCGC UGGGGAAAAGUUCAGAAGGUACCUGAGACACCUGUACAACAAGUGCCUGGCCGUCCUGU GUCUCCCGACCCGACUCUACUAAGAACCCAGAGUUCCUGCAUCUGACUCUGUGUAAUG CUCCUCCUGCAUUUUAUGUGCAAGAAAUACGGACCAGGUACCUGC

720-82-01 5'-

FIGURE 81A

Human Interleukin-1 beta (IL-18) Oligonucleotides

 $\tt gtaatttaatacgactcactatagggaaggtgcagttttgccaaggagtgctaaag-3'$

(SEQ ID NO:304)

562-15-01 5'-ctgattgaaatttatctaataaaacatcat-3'

(SEQ ID NO:305)

781-50-01	5'-TET-acttccaagctggc-3'	(SEQ ID NO:3	06)
781-50-02	5'-TET-gagagtggaccacac-3'	(SEQ ID NO:3	07)
781-50-03	5'-TET-gaatcagtgaagatgcc-3'	(SEQ ID NO:3	08)
781-50-04	5'-TET-cattgtaccatgaaatatcc-3'	(SEQ ID NO:3	09)
781-50-05	5'-TET-gaactttaatttcaggaattg-3'	(SEQ ID ⁰ NO:3	10)
781-50-06	5'-TET-ccctagtctgctagc-3'	(SEQ ID NO:3	11)
781-50-07	5'-TET-ttcaagtgtaacttattaacc-3'	(SEQ ID NO:3	12)
781-72-01	5'-TET-aagctggccgtg-3'	(SEQ ID NO:3	13)
781-72-02	5'-TET-tgcagttttgccaag-3'	(SEO ID NO-3	141

FIGURE 81B

Human Interleukin-1 beta (IL-18) (GenBank Accession #
M15330) (SEQ ID NO:315)

GGCAGAAGUACCUGAGCUCGCCAG<mark>UGA</mark>AAUGAUGGCUUAUUACAGUGGCAAUGAGGAUG ACUUGUUCUUUGAAGCUGAUGGCCCUAAACAGAUGAAGUGCUCCUUCCAGGACCUGGAC CUCUGCCCUCUGGAUGGCGGCAUCCAGCUACGAAUCUCCGACCACCACUACAGCAAGGG CUUCAGGCAGGCCGCGUCAGUUGUUGUGGCCAUGGACAAGCUGAGGAAGAUGCUGGUUC CCUGCCCACAGACCUUCCAGGAGAAUGACCUGAGCACCUUCUUUCCCUUCAUCUUUGAA GAAGAACCUAUCUUCUUCGACACAUGGGAUAACGAGGCUUAUGUGCACGAUGCACCUGU ACGAUCACUGAACUGCACGCUCCGGGACUCACAGCAAAAAAGCUUGGUGAUGUCUGGUC CAUAUGAACUGAAAGCUCUCCACCUCCAGGGACAGGAUAUGGAGCAACAAGUGGUGUUC UCCAUGUCCUUUGUACAAGGAAGAAAGUAAUGACAAAAUACCUGUGGCCUUGGGCCUC AAGGAAAAGAAUCUGUACCUGUCCUGCGUGUUGAAAGAUGAUAAGCCCACUCUACAGCU GGAGAGUGUAGAUCCCAAAAUUACCCAAAGAAGAAGAUGGAAAAGCGAUUUGUCUUCAA CAAGAUAGAAAUCAAUAACAAGCUGGAAUUUGAGUCUGCCCAGUUCCCCAACUGGUACA UCAGCACQUCUCAAGCAGAAAACAUGCCCGUCUUCCUGGGAGGGACCAAAGGCGGCCAG GAUAUAACUGACUUCACCAUGCAAUUUGUGUCUUCCUAAAGAGAGCUGUACCCAGAGAG UCCUGUGCUGAAUGUGGACUCAAUCCCUAGGGCUGGCAGAAAGGGAACAGÁAAGGUUUU AGGGUAGUGCUAAGAGGAUCUCCUGUCCAUCAGCCAGGACAGUCAGCUCUCUCCUUUCA GGCCAAUCCCCAGCCCUUUUGUUGAGCCAGGCCUCUCUCACCUCUCCUACUCACUUAA AGCCCGCCUGACAGAAACCACGGCCACAUUUGGUUCUAAGAAACCCUCUGUCAUUCGCU UUCAUUGGUCUAAUUUAUUCAAAGGGGGCQAAGAAGUAGCAGUGUCUGUAAAAGAGCCUA GUUUUUAAUAGCUAUGGAAUCAAUUCAAUUUGGACUGGUGUGCUCUCUUUAAAUCAAGU CCUUUAAUUAAGAQUGAAAAUAUAUAAGCUCAGAUUAUUUAAAUGGGAAUAUUUAUAAAA **UGAGCAAAUAUCAUACUGUUCA**

FIGURE 82A

Human Interferon gamma Oligonucleotides

448-59-01	5'-TET-GCATCGTTTTGGGTTCTCTT	(SEQ	ID	NO:316)
448-59-02	5'-TET-ACTTTAAAGATGACCAGAGC	(SEQ	ID	NO:317)
448-79-01	CACATTGTTCTGATCATCTG	(SEQ	ID	NO:318)
448-79-02	CGGTAACTGACTTGAATGTC	(SEQ	ID	NO:319)
448-79-03	TAGTAACTG GATAGTATCAC	(SEQ	ID	NO:320)
448-79-04	GACATTCAAGTCAGTTACCG	(SEQ	ID	NO:321)
498-20-01	AATTTAATACGACTCACTATACACATTGTTCTG	TCATO	CTG	
		(SEQ	ID	NO:322)
498-20-02	AATTTAATACGACTCACTATACGGTAACTGACTT	'GAATC	STC	
		(SEQ	ID	NO:323)
498-20-03	5'-TET-CACATTGTTCTGATCATCTG	(SEQ	ID	NO:324)
498-20-04	5'-TET-CGGTAACTGACTTGAATGTC	(SEQ	ID	NO:325)
498-40-01	5'-		•	·-
AGTAATTTACC	SACTCACTATAGGGACACATTGTTCTGATCATCTG	AAGA		
		(SEQ	ID	NO:326)
498-40-02	5'-			
AGTAATTTACC	GACTCACTATAGGGACGGTAACTGACTTGAATGTC	CAAC		
		(SEQ	ID	NO:327)
498-84-01	5'-TET-CATTCAGATGTAGCG	(SEQ	ID	NO:328)
498-84-02	5'-TET-GACTCATCAATCAAA	(SEQ	ID	NO:329)
498-84-03	5'-TET-GATTACAAGGCTTTA	(SEQ	ID	мо:330)

FIGURE 82B

Human Interferon gamma (SEQ ID NO:141)

CACAUUGUUCUGAUCAUCUGAAGAUCAGCUAUUAGAAGAGAAGAUCAGUUAAGUCCUUU GGACCUGAUCAGCUUGAUACAAGAACUACUGAUUUCAACUUCUUUGGCUUAAUUCUCUC GGAAACGAUGAAAUAUACAAGUUAUAUCUUGGCUUUUCAGCUCUGCAUCGUUUUGGGUUC UCUUGGCUGUUACUGCCAGGACCCAUAUGUACAAGAAGCAGAAAAACCUUAAGAAAUAUU UUAAUGCAGUCAUUCAGAUGUAGCGGAUAAUGGAACUCUUUUCUUAGGCAUUUUGAAG AAUUGGAAAGAGGAGAGUGACAGAAAAAUAAUGCAGAGCCAAAUUGUCUCCUUUUACUU CAAACUUUUUAAAAACUUUAAAGAUGACCAGAGCAUCCAAAAGAGUGUGGAGACCAUCA AGGAAGACAUGAAUGUCAAGUUUUUCAAUAGCAACAAAAAGAAACGAGAUGACUUCGAAA AGCUGACUAAUUAUUCGGUAACUGACUUGAAUGUCCAACGCAAAGCAAUACAUGAACUCA UCCAAGUGAUGGCUGAACUGUCGCCAGCAGCUAAAACGGGAAGCGAAAAAGGAGUCAG AUGCUGUUUCGAGGUCGAAGAGCAUCCCAGUAAUGGUUGUCCUGCCUACAAUAUUUGAAU UUUAAAUCUAAUUUAUUAAUAUAACAUUAUUUAUAUGGGGAAUAUAUUUUAGAC UCAUCAAUCAAAUAAGUAUUUAUAAUAGCAACUUUUUGUGUAAUGAAAAUGAAUAUCUAUU AAUAUAUGUAUUAUUUAUAAUUCCUAUAUCCUGUGACUGUCUCACUUAAUCCUUUGUUUU CUGACUAAUUAGGCAAGGCUAUGUGAUUACAAGGCUUUAUCUCAGGGGCCAACUAGGCA GCCAACCUAAGCAAGAUCCCAUGGGUUGUGUGUUUAUUUCACUUGAUGAUACAAUGAAC ACUUAUAAGUGAAGUGAUACUAUCCAGUUACUA

FIGURE 83A

Pneumocystis carinii (NUCLEODTIDES 84-415 OF ACCESSION # AF236872) (SEQ ID NO:331)

GAGGGUCAUGAAAGCGGCGUGAAAACGUUAGCUAGUGAUCUGGAAUAAAUUCAGAUUGC
GACACUGUCAAAUUGCGGGGAAGCCCUAAAGAUUCAACUACUAAGCAGUUUGUGGAAAC
ACAGCUGUGGCCGAGUUAAUAGCCCCUGGGUAUAGUAACAAUGUUGAAUAUGAAUCUUUU
GCGAGAUGAAAUGGGGGAUCCGCAGCCAAGUCCUAAGGGCAUUUUUUGUCUAUGGAUGCAG
UUCAACGACUAGAUGGCAGUGGGUAUUGUAAGGAAUUGCAGUUUUCUUGCAGUGCUUAA
GGUAUAGUCUAUCCUCUUUCGAAAGAAAGAGAAAGAGUAUAU

Candida albicans (NUCLEOTIDES 72-418 OF ACCESSION # X74272) (SEQ ID NO:332)

GGGAGCCAAAAGUAGGGACGCCAUGGUUUCCAGAAAUGGGCCGCGGUGUUUUUUGACCUGC
UAGUCGAUCUGCCCAGACGUAUCUGUGGGUGGCCAGCGGCGACAUAACCUGGUACGGGG
AAGGCCUCGAAGCAGUGUUCACCUUGGGAGUGCGCAAGCACAAAGAGGUGAGUGGUGUA
UCGGGGUUAAUCCCGUGGCGAGCCGUCAGGGCGCGAGUUCUGGCAGUGGCCGUCGUAGAG
CACGGAAAGGUAUGGGCUGGCUCUCUGAGUCGGCUUAAGGUACGUGCCGUCCACACGA
UGAAAAGUGUGCGGUGCAGAAUAGUUCCCACAGAACGAAGCUGCGCCGGAGAAAGCGAUU
UCUUGGAGCAAU

FIGURE 83B

Earwig R2 element (SEQ ID NO:333)

UAGGAUGAUAGCGCACCUGGUCAUCGUCUCU<mark>CUCAGCU</mark>GCUCACUUGCUGUUCUAAGUG A<u>UAAU</u>ACCGUUGUUUUUUUUAGUGGGUAUUCUUUUACGCUUUCGUAGGAGCGAGUCCCAC AC<u>UCUUGGA</u>GCA<u>AUCCG</u>GGGU<u>AGUGCCUAAAC</u>GCAUUUCUUCAACGU

Bombyx mori R2 element (SEQ ID NO:334)

GCCUUGCACAGUAGUCCAGCGGUAAGGGUGUAGAUCAGGCCCGUCUGUUUCUCCCCCGGA GCUCGCUCCCUUGGCUUCCCUUAUAUAUUU<u>UAACAUCAGAAACA</u>GACAUUAAA<u>CAUCUA</u> CUGAUCCAAUU<u>UCGCC</u>GGCGUACGGCCACG<u>AUCGGG</u>AGGGUGGGA<u>AUCUCG</u>GGGGUCUU CCGAUCCUAAUCCAUGAUGAUGACGACCUGAGUCACUAAAGACGAUGGCAUGAUGAUCC GGCGAUG